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May 25, 2003, 08:48:53 ; Search time 2746 Seconds (without alignments) 10958.595 Million cell updates/sec US-09-955-526-3 1034 I gagcaaacataacattgtct.....ataaggaaagttccttgtga 1034 4109280 Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 08
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Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 em_vi:*
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Unfect submission

Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, UGA

This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
c-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Lare cotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genset carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
closation/Qualifiers
lice //organism="Arabidopsis thaliana"
//db.xreff="Haxan:3702"
//dlone="136400"
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Eass. To 1066)
Feldmann, K.A., Volfcovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
                               ACCCAAGATATAATTGAGAAGGCACACCTTGGGGATTTGGACTACGTGAAGCATGCTCG 781
                                                                                                                                                                                              782 ACCCICITIACAGAITITIGITIGITITITIGIGGGAATATIAATCATAATGCTGAAGAAT 841
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/product=Bax inhibitor-1 like"
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Unpublished

(bases 1 to 1293)

Bolduc,N., Pitre,F. and Brisson,L.

Bordect Submission
Submitted (11-707-2001) Biochemistry and Microbiology, Laval
University, Quebec GIK 7P4, Canada
Location/Qualifiers

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FIL CDMA.
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Arabidopsis thaliana
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
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                                                                       Score 428.8; DB 8;
Pred. No. 1.6e-103;
0; Mismatches 197;
                                                                           41.5%;
                                                                           Query Match
Best Local Similarity 73.7
Matches 560; Conservative
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RESULT 3 AY091134 LOCUS

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Lee, Turages I. Chanh, M. Chang, C. H., Chang, E., Dale, J. M., Dang, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Coldsmith, A.D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Lam, B., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J. Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Satou, M., Seki, M., Shinn, P., Southwick, A., Satou, M., Seki, W., Ecker, J. R. and Theologis, A. Direct Submission Context Good Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, UGA RAFL cDNAe (RAFL CDNAe, TRIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAe (RAFL CDNA, TRIKEN Arabidopsis Full-Length CDNA): Seki, M., Narusaka, M., Ishida, J., Sakutu, M., Kamiya, A., Sakuta, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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SVGPIJKVALDVDPSILITAFVGTAIAFVCFSAAAMLARRREYLYLGGLLSSGLSMLM
WLQFASSIFGGSASIFKFELYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHSLTLFT
DFVAVFVRILIIMLKNSADKEEKKKKRRN"
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Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Boweer, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, Y., Ishida, J., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Niguyen, M., Palm, C.J., Shinozaki, K., Bavis, R.M., Seki, M., Shino, P., Southwick, A., Arabidopsis Full Length CDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yanada,K., Banh,J., Chan,M.M., Chang,E., Dale,J.M., Deng,J.M., Deng,J.M., Deng,J.M., Coldenith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yanamura,Y., Yu,G., Bowser,L., Chen,H., Greuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Myarsh,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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/gene="At5g47120"
/note="not present in genomic sequence"
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(Lambda ZAP) as a Xhol/Sstl insert. ecotype: Columbia"

1. .994

/gene="At5947120"

    .994
/organism="Arabidopsis thaliana"

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/chromosome="5"
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                                                                                                                                                     132 AACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACT 191
                                                                                                                                                                                           79 AGAAGCTGGAGCTATGATTCTCTTAAAACTTCCGTCAGATTTCTCCAGCCGTTCAGAAT 138
                                                                                                                                                                                                                                  CATCTCAAGCAGGTGTACCCTTACGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCT 251
                                                                                                                                                                                                                                                                                                                                                                                        312 ATGGTGTGGCTTCTCTGGTCCTTGTGAGGGAAAAAAGGGTGGCTCTTCTGATG 371
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                                                                             AAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGC 131
                                                                                                                22 AAAAAAAccaAAcAArddArdcGrrcrrcrrcrrcrrcrrcaAccrc---Gradc 78
                                         Gaps
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Query Match
41.3%; Score 427.2; DB 8;
Best Local Similarity 73.6%; Pred. No. 4.4e-103;
Matches 559; Conservative 0; Mismatches 198;
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197 C

BASE COUNT ORIGIN

Similarity

Query Match Best Local

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forganism="Arabidopsis thaliana"
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/db_sucetype="leaves"
/note="challenged with Pseudomonas syringae pv. tomato

DC3000::avrRPM1" 46. .789 /note="AtBI-1" /codon_start=1

SCO

College, Wye,

pathogen challenge Unpublished Sanchez, P., de Torres Zabala, M. and Grant, M. Direct Submission Submitted (24-NOV-1999) Biological Sciences, Wye (Ashford, Kent TN25-5AH, UK

JOURNAL REFERENCE AUTHORS TITLE JOURNAL 1006

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41.3%; Score 427.2; DB 8; 73.6%; Pred. No. 4.4e-103; live 0; Mismatches 198;
                                                                                                  Matches 559; Conservative
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(bases to 1006)
Sanchez, P., de Torres Zabala, M. and Grant, M. AtBI-1, a plant homolog of Bax inhibitor 1, suppresses Bax-induced cell death in yeast and is rapidly upregulated during wounding and
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/product="Bax inhibitor-1"
/produ
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Abobists thaliana AtBI-1 mRNA for Bax inhibitor-1, complete cds. AB025927.2 GI:7209773
AB025927.2 GI:7209773
Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
Arabidopsis thaliana
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Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; endicotyledoms; core endicots; Rosidee; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Kawai,M. and Uchimiya,H.

Direct Submission

Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,

Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,

Bunkuo-ku, Tokyo 113-0032, Japan

(B-mail:uchimiyadaimchns.iam.u-tokyo.ac.jp, Tel:81-3-3812-2910,

Fax:81-3-3812-2910)

On Mar 8, 2000 this sequence version replaced gi:6716123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawai,M., Pan, b., Reed, J.C. and Uchimiya, H.
Evolutionally conserved plant homologue of the Bax inhibitor-1
(BI-1) gene capable of suppressing Bax-induced cell death in
yeast(1)
PEBS Lett. 464 (3), 143-147 (1999)
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                           ACACAAGAGATTATAGAAAAGGCACACCTCGGTGACATGGACTATGTAAAACATTCGTTG
                                                                                              732 ACCCTITICACAGAITITIGGCGCTGTTTTTGTGCGCGATTCTGATCATCTTAAAGAAT
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Matches 559; Conservative 0; Mismatches 198; Indels
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/db_rref="taxon:3702"
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (Dases I to 775)

Yamada,K. Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,

Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,

Tang,C., Torviumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,

Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,

Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.J., Dam,B.,

Lin,J., Miranda,M., Narusaka,M., Nayven,M., Palm,C.J., Sakurai,T.,

Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,

Arabidopsis Open Reading Frame (ORF) Clones
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Yamada, Banh, W. Chang, C.H., Chang, E., Dale, J.M.,
Peng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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/protein_id="AAM$1107.1"
/d_xxref="G1:21280947"
/tzanslation="MDAPSSFFDSQPGSRSWSYDSLKNFRQISPAVQNHLKRVYLTLC
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SVGPLIKVALDVDPSILITATVGTATAFVCFSAAMIARRRFYLXLGGILSSGLSMLM
WLQFASSIFGGSASIFKFELYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHSLTLFT
DFVAVPYRILIIMLKNSADKEEKKKKRRN
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                                                                                                                                        Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA : 'RIKEN Arabletion and clustering of RAFL CDNA (RAFL CDNA : 'RIKEN Satcion'), Seti,M., Narusaka,M., Ishida,J., Satcio,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M., Chang, C.H., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Dass, Lin, J., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs. __iocation/Qualifiers
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kim, C., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T. Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A., Shinozaki, K., Direct Submission
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/db_xref="taxon:3702"
/chromosome="5"
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ecotype: Columbia"
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Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brarycora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Beknarycora, Viridiplantae, Streptophyta, eudicotyledons; core eudicots;
Rosidae; eurosids II, Brassicales; Brassicaceae; Brassica.
I baees I to 1010)
Bolduc, N. and Brisson, L.
Characcerization of Bax inhibitor I from Brassica napus
Unpublished
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Direct Submission
Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval University, Quebec GIK 7P4, Canada
Location/Qualifiers
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                               GCAAGGCGCAGGGAGTACTTGTACCTTCGGGGGCCTTCTTTCATCTGGCGTCTCCCTTCTC
TCAGCTCCTCCTTATCAAGAGCAAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACTTTTT
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Brassica napus Bax inhibitor 1 (BI-1) mRNA, complete cds.
AF390555
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/organism="Brassica napus"
/cultivar="Westar"
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/codon_start=1
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/translation="MDSFSSFPDSQPGSRSWSYDSLKNLRQISPSVQNHLKRVYLTLC
CALVASAFGAYLHVLWNIGGILTTIGCFGSMIWLLSCPPYEQQKRLSLLFLSAVLEGA
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WLQFASSIFGGSASIFYFELYFGLLIFYGYMVVDTQDIIEKAHLGDMDYVKHSLTLFT
DFVRVFVRVLIMLKNSADKERNN"

1 203 c 232 g 331 t
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370 agirgarrirgacccaagcarccicarcacceccirirgicgaacrgcgaraccrirnar 429 CTGTTTCTCAGGGGCAGCGATGTTGGCAAGACGCAGAGAGTACCTCTACCTCGGAGGACT TTGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCT 430 482

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AF453320 AF453320.1 LOCUS DEFINITION ACCESSION VERSION KEYWORDS RESULT 8 AF453320

AF453320 1013 bp mRNA linear PLN 27-DEC-2001 Brassica oleracea bax inhibitor-like protein (BII) mRNA, complete GI:17981373

/gene="BII" /note="may be involved with programmed cell death; similar to Arabidopsis thaliana and Homo sapiens bax inhibitor" Tracheophyta; death Private Bag The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSD1 and B1: their role during cell Brassica oleracea Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracl Bukaryota, Viridipliophyta, eudicotyledons, core eudicot Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica I (bases I to 1013) Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and Bason, J.R. and senescence
Unpublished
(Chases I to 1013)
Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. Research, Submitted (29-NOV-2001) Crop and Food Palmerston North 5301, New Zealand Location/Qualifiers 1. .1013 /organism="Brassica oleracea" /boxref="taxon:3712" 1. .1013 Brassica oleracea Direct Submission source BASE COUNT ORIGIN SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL AUTHORS JOURNAL REFERENCE CDS FEATURES TITLE

3; Gaps AGAAGAAGAAGAAGATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCA DB 8; Length 1013; Indels Score 413.4; DB 8; Pred. No. 2.1e-99; 0; Mismatches 206; Query Match
Best Local Similarity 72.5%;
Matches 550; Conservative

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/prodein_id="bax inhibitor-like protein"
/protein_id="AAL50980.1"
/db_xref="G1:17991376"
/translation="WESFSSFFDSQPGSRSWSYESLKNIHQISPSVQNHLKRVYIJI.C
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SVGPLIKVAVDFDPSILITAFVGTAIAFICFSGAAMLARRREYLYLGGLLSSGLSMLM
WLQPASSIFGGSASIFKFELYFGLLIFVGYMVVDTQEIIEXAHLGDMDYVKHALTLFT
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mRNA, complete
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II, Brassicales, Brassicaceae, Brassica.
1 (bases I to 1019)
Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and
Eason, J.R.
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                                                                     478 GCTTGTCCATGCTTATGTGGCCTTCAGTTTGCCTCTTCCATCTTTGGTGGCTCTGCATCCA 537
418 GGGCAGCGATGTTGGCAAGACGCAGAGAGTACCTCTACCTCGGAGGACGACGTTCTTCATCTG
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2 (bases 1 to 1019)
Coupe,S.A., Sinclair,B.K., Watson,L.M., Bucknell,T.T. and
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Brassica oleracea bax inhibitor-like protein (BI2)
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Submitted (19-NOV-2001) Crop and Food
Palmerston North 5301, New Zealand
Location/Qualifiers
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/organism="Brassica o.
/db_xref="taxon:3712"
1. _1019
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Kawai,M., Pan,L., Reed,J.C. and Uchimiya,H.

Evolutionally conserved plant homologue of the Bax inhibitor-1
(BI-1) gene capable of suppressing Bax-induced cell death in yeast(1)
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Bax inhibitor-1.
Oryza sativa (strain:Yamahoushi) cDNA to mRNA.
Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
Pred. No. 1.3e-95,
0; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790 ATGCATCTGAGAAGGAAGAGAAGAAGAAGAAGAGGA 825
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AB025926
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/protein id="C037797.1"
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LASSAVGASTAHIALNIGGMLTMLACVGTIAWMFSVPVYERRRFGLLMGAALLEGASU
GPLIELAIDFDPSILVVGFVGTALTAFGCFSQAAIJAKRREYLYLGGLLSSGLSJLLML
QFVTSIFGHSSGSFMFEVYFGLLIFLGYMVYDTQEIIERAHHGDMDYIKHALTLFTDF
VAVLYRYLIIMLKNAGDKSEDKKKRRRGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAX inhibitor 1, pBI-1 gene.
Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuckelhoven, R., Dechert, C., Trujillo, M. and Kogel, K. H. Differential expression of putative cell death regulator genes near-isogenic, registant and susceptible barley lines during interaction with the powdery mildew fungus Plant Mol. Biol. 47 (6), 739-748 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 CGTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACT 162
                                                                                                                               726
                                                                                                                                                                                                                                                                         727 CATTGACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAA 786
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Submitted (22-JAN-2001) Hueckelhoven R., Institute for
Phytopatholgy and Applied Zoology, Justus-Liebig-University
Glessen, Heinrich-Buff-Ring 26-32, 35392 Glessen, GERMANY
Location/Qualifiers
                                                               646 cciscascritchreiridaderriacriridaccieiridarcriccridaderakchiderer
                                                                                                                                      TTGACACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGGATTACGTTAAGCATG
                                                                                                                                                                                                  607 IGGCIGITIICAAGITIGAGITIGIAJITIGGACICTIGGIGIJITIGGGCIACAICGICI
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Hordeum vulgare mRNA for BAX inhibitor 1 (pBI-1 gene)
AJ229421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 744.
|gene="pBI-1"
|function="putative cell death suppressor"
|codon start=1
|product="BAX inhibitor 1"
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(cultivax="Pallas")
(db xref="taxon:112509"
(tissue_type="leaf")
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llarity 67.4%; Pred. No. 3.1e-81;
Conservative 0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                   787 AGAATGCATCTGAGAAGAGAAGAAGAAGAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          826 AGAACGCGTCTGACAAGTCGGAGAGAGAAGAAGAAGA 864
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1. .744
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Hueckelhoven, R.
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Matches 487;
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CVALAASAYGAYLHVALNIGGMLTMLGCVGSIAWLFSVPVFBERKRFGILLAAALLEG
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IMLQFAASIFGHSTGSPMFEVYFGLLIFLGYNVYDTQEIIERAHHGDMDYIKHALTLF
TDFVAVLVRILVIMLKAASDKSEEKKRKKRS"
295 c 317 g 307 t
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                                                                   Codes 1 to 1181)

Kawai, M. and Uchimiya, H.

Direct Submission
Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,
Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,
Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,
Enst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,
Sunco-ku, Tokyo 113-0032, Japan
(E-mail:uchimiyaeèmchen iam.u-tokyo.ac.jp, Tel:81-3-3812-2910,
Fax:81-3-3812-2910)
On Mar 8 2000 this sequence version replaced gi:6759252.
Sequence updated (02-Mar-2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 CATCTGGCGTCTCCCTTCTCTGGTTGCACTTTGCATCTCCACATTTTTGGTGGTTCCA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 Agagagagagagagagagaganganggaggcchichachcgachcgroggcgracgaggg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 cecceaececrececraceacraceacrecereaacaacriceccaearcrecececececere 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="Bax inhibitor-1"
/protein_id="BAA89540.3"
/db_xref="GI:7209772"

    ..1181
/organism="Oryza sativa"
/strain="Yamahoushi"
/db_xref="taxon:4530"
1...1181

       Lett. 464 (3), 143-147 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BI-1"
126. .875
/gene="BI-1"
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/dlone="RZ957"
/clone lib="eticlated leaf tissue of rice"
/clone lib="eticlated leaf tissue of rice"
/note="Westor: Lambda ZAP II/pBluescript, V-type: Plasmid;
A Lambda ZAP II/DNA library was constructed from mRNA
Extracted from eticlated leaf tissue of the rice cultivar
'IR3' and converted to pBluescript (amp resistant) as
described in Causse et al. (1994) Genetics 138:1251-1274.
For insert amplification, Use MI3 forward and reverse
primers. Restriction site is ECORI. Clones from this
library are designated with the prefix 'RZ'."
<11. .418
9 a 118 c 124 g 116 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is a partial sequence of the RFLP clone named above that was mapped at Cornell University Plant Breeding Dept. and sequenced at the Genome Sequencing Center at Cold Spring Harbor Laboratory. This marker is located on rice chromosome 2. For citations and other related information concerning this probe, please refer to the Gramene database at http://www.Gramene.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 IGCIGGGGCTIACCITCACATICIAGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 CATGGGAAGCATGGTGTGTTCTCTCTCAGCTCCTTATCAAGAGCAAAAAAGGGTGGC 361
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                           Email: srm4@cornell.edu
Primer A: M13 universal Forward GTAAAACGACGGCCAGT
Primer B: M13 Universal Reverse AACAGCTATGACCATG
STS size: 418
Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/cultivar="IR36"
/db_xref="taxon:4530"
/map="2"
                                                                                                                                                                                                                                                                                                                                                                                         5units
                                                                                                                                                                                                                                                      Template: 20-100ng
Primer: 5pmol each
DNTPs: 40nmol
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Total volume: 50ul
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KCl: 500mM
MgCl2: 15mM
Gelatin: 0.1%
PH: 8.3
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Matches 262, Conservative
Fax: 6072556683
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DNTPs: 4
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1 (bases 1 to 418)
McCouch, S.R.
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                                                                                                                                                                                                                                                                                                              128 TTGCACTGGCCTCATCTGCCGTGGGTGCTTACCTACATTGCCCTGAACATCGGCGGGA 187
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67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TGCTGACAATGCTCGCTTGTGTCGGAACTATCGCCTGGATGTTCTCGGTGCCAGTCTATG
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CCTTCTACTCGACCTCGTCGGCGGCGGCGAGCGGCTGGGGCCACGACTCCCTCAAGAACT
                                                                                   163 TCCGCCAGATCTCACCTCTCGTTCAACTCATCTCAAGCAGGTGTACCTTACGCTATGCT
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Cornell University
Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
Tel: 6072550420
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Oryza sativa
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REFERENCE AUTHORS TITLE JOURNAL COMMENT

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892 bp mRNA linear PRI 27-NOV-1997
Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA,
AP033095
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/gene="TBGT"
/note="Small transcript; similar to human TEGT large
transcript encoded by GenBank Accession Number X75861 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 892)
Cowling,R.T. and Birnboim,H.C.
Direct Submission
Submitted (05-NOV-1997) Cancer Research Group, Ottawa Regional Cancer Centre, 501 SWHA Road, Ottawa, ON KIH 816, Canada
                                  240 AGAGGGGCACCGTGGGGACATGGACTACATCAAGCACGCGCTGACTCTTCTTCACCGACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTCATCTAAGCAG 203
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                                                                                  748 ȚIGGCGCTGTȚIȚIGTGCGGATICTGAICAICATGTȚAAAGAAIGCAICTGAGAAGGAAG 807
                                                                                                                    180 TIGITICGGIICTIGITCGAATCCITGICATCATGAGAATGCACAGGAGAATCCC 121
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    Query Match 12.1%; Score 125.2; DB 9; Length 892; Best Local Similarity 52.2%; Pred. No. 1.9e-22; Matches 358; Conservative 0; Mismatches 313; Indels 15;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE #207657"
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/gene="TEGT"
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Homo sapiens
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                                                                                                                                          G71526
360 bp DNA linear STS 08-JUN-2001
A61521534FMo17 maize leaf DNA Zea mays STS genomic, sequence tagged
                                                                                                                                                                                                                                                            Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 360)
1 (bases 1 to 360)
3' UTR sequences of maize genes
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 TCTACTTTGGCCTCCTGGTTTTCCTGGGATATATGTGTTTTGACACCCAGGAGATCATCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 TCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCTGTTTTTCAAGTTTGAGT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TCTGGCTGCAGTTTGCTACTTCAATCTTTGCCCACAGCGGGAACCTTCATGTTTGAGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 IGTATTTTGGACTCTTGGTGTTTTGTGGGCTACATCGTCTTTGACACCCAAGAAATTATTG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="DEB11"
/db_xref="taxon:4577"
/clone_lib="maize leaf DNA"
/note="PCR products amplified from genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%; Score 137.2; DB 11; Length 360; 70.2%; Pred. No. 1.3e-25; tive 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
542 TCTTTCATCTGGCGTCTCCCTTCTTCTGGTTGCACTTTGC 583
542 TCTTTCATCTGGCGCTCTCCCTTCTCTGGCTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTGC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-229
Fax: 515-294-229
Email: schnable@iastate.edu
Primer A: CAATTCATTCAGCAGCTACC
Primer B: CGACTTGTTATTGACTAGG
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer: each 0.5 um
dNTPs: each 200 um
Tag Polymerase: 0.05 units/ul
Total vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermal cycler: Perkin Elmer TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MgC12: 2 mM
KC1: 50 mM
Tris-HC1: 20 mM
Pr: 8.4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Schnable, P.S. Schnable laboratory
                                                                                                                                                                                   G71526
G71526.1 GI:14333211
STS.
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a 87 c
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Matches 184; Conservative
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BASE COUNT
ORIGIN
                                                                                                 RESULT 13
G71526/c
LOCUS
DEFINITION
                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/codon_start=1
/producl="testis enhanced gene transcript"
/protein_id="AAH00916.1"
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LEFCIAVNPSILPTAFWGTAMIFTCFTLSALYARRRSYLFLGGILMSALSLLLISSLG
NVFFGSIWLFQANLYVGLVVMCGFVLFDTQLIIEKAEHGDQDYIWHCIDLFLDFITVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 GIGIACCITACGCIAIGCIGIGCTITAGIGGCAICGGCIGCIGGGGCTIACCITCA--- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GICTAIGCAAGITIIGCCCCTIGIAIGITIGIGGCGGCIGCAGGGGCCTAIGICCAIAIG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTTCTCTCAGCTCCTCTTATCAAGAG-----CAAAAAAGGGTGGCTCTTCTGATG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 GITITCAAGITIGAGITGIATITIGGACICTIGGIGITIGIGGGCIACAICGICITIGAC 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690 GATCTCTTCTTAGATTTCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 --CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2609,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 125.2; DB 9; Length 52.2%; Pred. No. 1.8e-22; ive 0; Mismatches 313; Indels
                                                                                        /db_xrefe"taxon:9606"
/dlone="MGC:5230 IMAGB:2900280"
/tlssue_type="Hacenta, choriocarcinoma"
/lab_host="NIH MGC_10"
/lab_host="DH10B"
/note="Vector: pGWV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 776 t
                                             organism="Homo sapiens"
Ab xref="LocusID:7009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKLMMILAMNEKDKKKEKK"
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Location/Qualifiers
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Matches 358; Conservative
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                             source
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Contact: villalon.D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://lmage.llml.ggv
Series: IRAK Plate: 3 Row: k Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2645728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Submitted (16-NOV-2000) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                        450 crcagiócacriciardecadecedeseracriacererereseaderarerreas 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 ACTCAACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCACTGCATT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 GATCTCTTCTTAGATTTCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT 746
                          431
                                                                        330 dearridearrecriacadeagringecerodecerecerodadririgiarineerore 389
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                          372 GCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Search completed: May 25, 2003, 11:00:16 Job time : 2754 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	-	Description	Arabidopsis thalia	Arabidopsis thalia	Testis Enhanced Ge	Testis Enhanced Ge	Arabidopsis thalia	Bovine mammary tis	Lung cancer, associ	Human cDNA differe	Bax inhibitor BI-1
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		e E	24	21	22	22	21	22	21	24	13
	Query	Length	1009	1066	884	527	712	873	2922	2600	2634
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ALIGNMENTS

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Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress; disease; crop; thale cress; tolerance factor; insect; pathogen; nutrition; ds.
                                                                       Arabidopsis thaliana expressed polynucleotide SEQ ID NO 223.
                ABN98455 standard; DNA; 1009 BP.
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AN Y.
HAMILTON C M.
PRICE J L.
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PAGE A.
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LEDFORD B L.
WOESSNER J P.
HAAS W D.
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KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                          HURBAN P.
                               Gorlach J, Rameaka JG,
Garcia CA, 1
Hurban P;
        (HAAS/)
(GARC/)
(KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
                          HURB/)
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The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN99231-ABN99231), given in the specification or lits fragment. A polypeptide (II) encoded by given in the specification or lits fragment. A polypeptide (II) encoded by given in the specification or lits fragment. A polypeptide (II) encoded by given in the specification or lits fragment. A polypeptide or a cid, is useful for screening a candidate agent for its biological effect. (I) is useful for screening a candidate agent for related genes, in producing compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression or function of its encoded compositions that modulate the expression of protein. Manaping functional regions of the protein and in studying associated physiological pathways. (I) is also useful in studying asceneing assays of various plant strains to determine the strains that care best capable of witheranding a particular disease or environmental care best capable of witheranding agents, insectional for screening of biologically active agents, insectional agents, insection of capacity in proved methods of treating production or than early on useful in a companion or a particular plant, for identifying other mediators that may induce that colerance to environmental stress. (I) is also useful or any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that may induce to losynthetic pathways of nutritional commercial, or medicinal value and biosynthetic pathways of nutritional commercial or medicinal or compounds that may affect the biological function of the gene or gene products or contenting or may affect the biological function of the gene or gene products or the se New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein Hamilton CM, Price JL, Raines TM, Yu Y, A, Mathew AV, Ledford BL, Woessner JP, Haas M, Slater T, Davis KR, Allen K, Hoffman N, Claim 1; SEQ ID NO 223; 49pp + Sequence Listing; English ecification, but was obtained in electronic format esegdata.uspto.gov/sequence.html?DocID=999909770445 An Y, Hamil Page A, Ma Kricker M, WPI; 2002-400781/43.

Sequence 1009 BP; 243 A; 201 C; 218 G; 347 T; 0 other;

ä 3; Gaps Query Match

41.5%; Score 428.8; DB 24; Length 1009;
Best Local Similarity 73.7%; Pred. No. 4.1e-115;
Matches 560; Conservative 0; Mismatches 197; Indels 3;

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132 AACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACT 191 셤

619 731 679 259 319 559 671 ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791 680 Accertricacreaertreraderererirerresearrereareareireaasaa 739 311 371 431 379 491 439 551 499 611 80 AGAAGCTGGAGCTATGATTCTCTTAAAACTTCCGTCAGATTTCTCCAGCCGTTCAGAAT 139 GCGTCTGCTGTTCTTGAAGGTGCTTCTGTTGGCCCCCTTGATCAAGTGGCAATTGATGTT 252 TACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGC <u>raccircoargiocircigaaanarcagcagraniciraacaacaaricaariragaacr</u> ATGGTGTGGCTTCTCTCAGCTCCTTATCAAGAGCAAAAAAGGGTGGCTCTTCTGATG GCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC 380 GACCCAAGCAICCITAICACTGCGITIGITGGAACTGCGATAGCGTTTGTCTGTTTCTCA GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT 500 GGCTIGTCTAIGCTAATGTGGCTCCAGTTTGCCTCTTCGATCTTTGGTGGCTCTGCATCT CATCITAAACGGGTTTATTICACCTTATGTTGTGTGTCTTGTGGCGTCTGCCTTTGGAGCT 260 Argarriegerecirreargieciecirargaacaccaaaaaagerrrererererr GATCCAAGCATTGTGTTTGCGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGGTTGCTTCTCA 440 geageageaargrinageaagaegeaggagiarereraceringaaggaererinearer GGCGTCTCCCTTCTCTGGTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT 612 GITITICAAGITIGAGITGIATITIGGACICITIGGIGITIGIGGGCTACATCGICITITGAC sso arcriraagrirgagrigiacririgaacririgaarcririgiagaaracargargargaac 620 acacaadaatraracaaaaddcacaccrccgrcacarddacardarcrargraaaacarrcgrrd CATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCT Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence, ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 21973 740 TCAGCAGATAAAGAAGAAGAAGAAGAAAAAGGAGAAACT 779 792 GCATCTGAGAAGGAAGAAGAAGAAGAAGAGGAGAAACT 831 99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. AAC38715 standard; DNA; 1066 25-FEB-2000; 2000EP-0301439. 17-OCT-2000 (first entry) Arabidopsis thaliana 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; EP1033405-A2 25-FEB-1999; 06-SEP-2000 AAC38715; 200 320 (552 (732 672 372 432 492 192 140 312 RESULT 2 AAC38715 à ò d g δ ઠે 셤 g à δ g g à d 8 g ö q à

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                                                                                                                                                                                                                                                                                                                                         AAF44782 standard; cDNA; 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.3%; Score 416.8; DB 21; Length 1066; llarity 73.6%; Pred. No. 1.4e-111; Conservative 0; Mismatches 197; Indels 4;
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99US-0161404.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161360.
99US-0161920.
99US-0161992.
99US-0161993.
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99US-0159329.
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Matches 559; Conserv
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28-OCT-1999;
28-OCT-1999;
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The present invention relates to coding sequences (see AAP44740-F44840 and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
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                                                                            630 Acadaagahtharadaaaaagdcacaccccogigacargagactargraaaacarrcorrd
Query Match
21.4%; Score 221.2; DB 22; Length 884;
Best Local Similarity 60.6%; Pred. No. 2.6e-54;
Matches 383; Conservative 0; Mismatches 243; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell death modulator; programmed cell death; PCD; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Testis Enhanced Gene Transcript protein coding sequence #1
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                                                                                                                                                                                                                                                                                                                                        792 GCATCTGAGAAGAAGAAGAAGAAGAAGAGAGAGAAACT 831
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Novel defender against cell death polynuclectide useful for modulating programmed cell death pathway and specific development pathways in forestry plant ,
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64 ICTGTTGAATATTGGAGGGCTCCTCACGGGGCTCGCTTGCATTGGTTCTGTAATCGGGCT 123
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                                                                                                                                                                                                                                       184 recrecerroa a de de conservados de conseces de conservados de conservados de consecuencia 
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                                                                                                                  TGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTCGATCC
                                                                                                                                                                                                                                                                                                     AAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGTTGCTTCTCAGCTGC
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P-PSDB; AAB65756.
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                                                                                                                                                                                                                                                                                                                                       141 gcaaggggagggagggagarrccrcaagaacrrcggccagararcrccggggggar 200
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                                                                                                                                                                                                                                                                                                                                                                                          CTCACCTCAAGAATGTTTATCTGTCCTTATGCTGTGCCTTGATGGCTTCGGCCGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAA
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                                                                                                                                                                                                                                  21.2%; Score 219.2; DB 22; Length 527; ilarity 74.5%; Pred. No. 7.7e-54; Conservative 0; Mismatches 98; Indels 1;
                                                                                                                                                                                                   Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 70058.
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                Claim 1; Pages 62-63; 142pp; English
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99US-0123180.
99US-0123548.
99US-0125788.
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                                                                                                                                                                                                                                                     Best Local Similarity
Matches 289; Conserv
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05-MAR-1999;
09-MAR-1999;
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New polypeptides and polynucleotides encoding the polypeptides, which mare expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting angiogenesis and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 873 BP; 206 A; 218 C; 196 G; 253 T; 0 other;
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gland; cancer; tumour; angiogenesis;

Bovine; mammary

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Grigor MR, Molenaar AJ;

Havukkala IJ, Gleen M,

GENESIS RES & DEV CORP LID. NEW ZEALAND PASTORAL AGRIC RES INST LTD.

23-AUG-2000; 2000WO-NZ00166

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cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; yprecological; antiinfective; yprecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer associated gene sequences, referred to as lung cancer gens, useful for treatment, prevention, and diagnosis of disorders
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535 CITITCCAGGCAAACCIGTATATGGGGCTGGTGGTCGTGTGGCTTTGTCCTTTTTGAT 594
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                                                                                          654
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                                                                                                                                                                                                                                          715 G-----AGAAGGATAAGAAGAAGAAGTGAAGCAGCCATCCAGCCTTGCCCAATTTG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; lung cancer associated protein; neuroprotective; cytostatic;
                                                                                                                                                                   655 gaccirciiciigaariicgiaaciciciicagaaagcicaigaigaicciggciaigaai
                                                      732 ACCCITTICACAGAITITIGGCGCTGITITIGIGCGGAITCTGAICAICAIGTAAAGAAI
                                                                                        595 ACTCAACTCATTATTGAAAAGGCTGAAAATGGAGATAAAGATTATATCTGGCACTGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer associated polynucleotide sequence SEQ ID 73.
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such as lung cancer
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disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polymucleotide sequences AFF18455 - AFF18433 and peptide AABS6849 are used in the course of the invention for the identification and characterisation of the polymucleotide and protein
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                                                                                                                                 Score 125.2; DB 21; Length 2922;
Pred. No. 6.5e-26;
0; Mismatches 313; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, 88, granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
                                                                                                   Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;
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Matches 358; Conservative
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Beazer-Barclay Y, Weissman SM,
                drug toxicity
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rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. iungal infection; sterile inflammatory disease; psoriasis; Vockley J; 03-OCT-2001; 2001WO-US30821. 03-OCT-2000; 2000US-237189P (GENE-) GENE LOGIC INC 40200228999-A2 Homo sapiens. 11-APR-2002

expression Detecting granulocyte activation by detecting differential expressiof genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and Yamaga S, WPI; 2002-435328/46

Claim 1; SEQ ID No 1229; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by the chip analysis as given in the specification, and comparing the expression level in an unactivated of GCA, where differential expression level in an unactivated GC, where differential expression of Gs is indicative of GCA and that alters the expression of Gs is indicative of GCA with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating (M3) is unallered response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allered response in a subject or a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the cheer lof expression in a sample of the tissue of gene (s) from GS, where the level of expression of the gene is indicative of inflammating (M3) an inflammation (especially chronic) or in a tissue, an allered cesponse in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammatory disease, by contacting a tissue having of the detecting an inflammation in a subject, exposure of a subject to a pathogen or sterile for greening an inflammation in a tissue, an allergic cesponse in a subject, exposure of a subject to a pathogen or sterile of from GS in the tissue, M1 is useful for screening an agent capable of modulating GCA preferrably in an inflammation in a tissue, M2 is useful for creening an inflammation in a subject, exposure of a subject to a pathogen or sterile response in a subject, exposure of a subject to a pathogen or sterile conformation of the above ond distance reperfusion injury, ARDS, adult respiratory distance or inflammatory bowel disease, also bacterial infection, protozol infection, viral infection, protozol infection, viral infection in generative or inflammatory because defificati of the printed specification, but was obtained in electronic cormat directly from WIPO at ftp.wipo.int/pub/published_pct_sequences The sequence data for this patent

Score 122; DB 24; Length 2600; Pred. No. 5.3e-25; 0; Mismatches 315; Indels 15; Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other; Query Match
Best Local Similarity 51.9%;
Matches 356; Conservative

317 259 247 371 487 611 544 671 731 791 724 127 GICTATGCAAGITTTGCCCTTTGTATGTTGTGGCGGCTGCAGGGGGCCTATGTCCATATG 187 307 431 367 491 427 551 545 CCTTTCCAGGCAAACCTGTATGTGGGACTGGTGGTCATGTGTGGCTTCGTCCTTGTTGAT 604 664 144 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG --CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG 188 GICACICATITCATICAGGCIGGCCIGCIGICTGCCTIGGGCICCCIGATATIGATGATT TGGCTTCTCTCAGCTCCTCCTTATCAAGAG-----CAAAAAAGGGTGGCTCTTCTGATG rescrieareschachecrearasechrehancreanehahahahaerrescrierrecr egarriecarrectracaddagriegecreddecereceredagrirrerararectere 368 AACCCCAGCATCCTTCCCACTGCTTTCATGGCCACAGCAATGATCTTTACCTGCTTCACC 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCT CICAGIGCACICIATGCCAGGCGCCGIAGCIACCICITICIAGGAGGIAICTIGAIGA GGCGTCTCCCCTTCTCTCTGCTTGCACTTTGCATCCTCCATTTTTGGTGGTTCCATGGCT GCCCTGAGCTTGTTTGTCTTCCCTGGGGAAT --- GTTTTCTTTGGATCCATTTGG GTTTTCAAGTTTGAATTGTATTTTGGACTCTTTGGTGTTTTGTGGGCTACATCGTCTTTGAC 732 ACCCTTTTCACAGATTTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 665 garcircircinadairircarracicircircagaaacicardaigaiccidgccardaar rrigargegerrrraaaarrrrereararaeceeereaaegeageaeereaaea GTGTACCTTACGCTATGCTGTGCTTTTAGTGGCATCGGCTGCTGGGGCTTACCTTCA----GATCCAAGCATTGTGTTTTGGCGCTTTTTGTAGGTTGTGCTGTGGTTTTTTGGTTGCTTCTCA GCAGCTGCACTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC Bax inhibitor; BI-1; human; apoptosis; ss. GCATCTGAGAAGGAAGAAGAA 817 Location/Qualifiers 725 GAAAAGGATAAGAAGAAAAAGAGAA 750 AAV59067 standard; cDNA; 2634 98WO-US05015. 02-FEB-1999 (first entry) Bax inhibitor BI-1 cDNA. Homo sapiens WO9840397-A1 13-MAR-1998; 17-SEP-1998 AAV59067; 128 318 372 308 428 488 672 605 89 204 260 248 432 552 612 792 RESULT 9 AAV5906 g 셤 셤 g ∂ 셤 g à a $\dot{\delta}$ ઠે ਨੇ g ò 셤 à g 셤 $\dot{\delta}$ ઠે ò 셤 δ

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                                                                                                                                                                                                                                                                                                  This cDNA clone codes for an inhibitor protein, termed BI-1 (see AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding BI-1 and BI-2 (see AAV5968) were identified by suppression of Bax-induced death of yeast cells transformed to express human Bax. A human Hep62 cDNA library was used for library screening. The invention provides vectors, optionally expression or viral vectors, containing BI nucleic acids, and host cells containing these vectors. The nucleic acids encoding BI-/PI-2 can be used to increase expression of these proteins in cells, or antisense molecules prepared from them used to decrease expression. In these ways, cellular apoptotic activity may be modulated (claimed). The nucleic acids and complementary sequences are also useful as probes to detect BI-encoding nucleic acid molecules in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 51.9%; Pred. No. 5.4e-25;
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps
                                                                                                                                                                          Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate cellular apoptotic activity or identify agents altering BI-1 or BI-2 binding which can modulate apoptotic activity
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                                                                                                                                                                                                                                                                       Claim 2; Page 61-63; 80pp; English.
  97US-0818514.
                                        (BURN-) BURNHAM INST
                                                                                                                      WPI; 1998-531519/45
                                                                                                                                            P-PSDB; AAW73136
                                                                                Reed JC, Xu Q;
14-MAR-1997;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABP6111-ABD56305), and also encompasses polypeptides 90% identical and polymotechides 93% identical to the sequences of the invention. The invention additionally relates to to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymoteleotides and polypeptides in diagnosing, or polymoteleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system cancer (e.g., infections ovarian cancer and dysmenorrhoea), anovalation, collosofers (e.g., chock syndrome, ovarian cysts, opportives, and toxic disorders, infections (e.g., chock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and cyaintis), immune disorders (e.g., congenital and acquired immunodeficancies, autocimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pcOs; ovarian cyst; dysmenornhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                    756
637 ACTCAACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCACTGCATT 696
                                         ACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                    GATCTCTTCTTAGATTCCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HPDWT56 cDNA, SEQ ID NO:1953.
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                                                                                                                                GCATCTGAGAAGGAAGAAGAA 817
                                                                                                                                                                         GAAAAGGATAAGAAGAAAGAGAAGAA 782
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                                                                                                                                                                                                                                                                                 ABQ56073 standard; cDNA; 751
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                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological diseases
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Human secreted protein 5' EST, SEQ ID NO: 8293

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Giordano J;

Duclert A,

Dumas Milne Edwards J, WPI; 2000-500381/45.

(GEST) GENSET 26-FEB-1999;

21-FEB-2000; 2000EP-0200610.

EP1033401-A2 Homo sapiens

06-SEP-2000.

99US-0122487

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invention.
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respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and abolynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, dung targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;

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512
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                                                                                                 16;
8.1%; Score 83.8; DB 24; Length 751; 50.6%; Pred. No. 4.3e-14; vative 0; Mismatches 288; Indels 16
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                                                         Best Local Similarity 50.63
Matches 312; Conservative
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ВP

AAC04218 standard; cDNA; 380

(first entry)

06-OCT-2000

AAC04218;

RESULT 11
AAC04218
ID AAC04
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AC AAC04
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Pred. No. 3e-12;
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Similarity 53.7%;
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Best Local Similarity 53.74
Matches 180; Conservative
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188 TGATGATCCTGGCCATGAATGAAAGGATAAGAAGAAGAAGAGAGAA 143

AAV86028 standard; cDNA; 520 BP

RESULT 13 AAV86028

g

(first entry)

27-APR-1999 AAV86028;

EST clone B115.

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expressed in cancer tissues. ABB/993 to ABB/9004 represent proteins encoded by the ABG6076 to ABG60787 nucleic acid sequences. (I) can be used in antisense therapy, An antibody immunoreactive with a polypebtide used in antisense therapy. An antibody immunoreactive with a polypebtide for detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probefyziner derived trom (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the presence of cells in a sample hybridises to (I), and for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise the proposites, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dwivedi P, Molino GA;
                                                                                                                                                                                      Human, colon cancer, cancer, tissue profiling, forensic, mapping, genetic analysis, diagnostic, antisense therapy, gene; ss.
                                                                                                                                                Human colon cancer related nucleotide sequence SEQ ID NO:2922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 74; DB 24; Length 595; 58.0%; Pred, No. 2.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 595 BP; 180 A; 124 C; 130 G; 155 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carroll E,
                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 796pp; English.
                    9227/c
ABQ59227 standard; cDNA; 595
                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2000; 2000US-237271P
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.0
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burgess C, Astle JH,
Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-426115/45.
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                                                                                                                                                                                                                                                                                          40200229086-A2
                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                              02-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                         ABQ59227;
RESULT 12
ABQ59227/c
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New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pitultary, retina and colon cDNA libraries

Merberg D;

Lavallie ER, McCoy JM, Treacy M;

98WO-US06954. 97US-0835913.

10-APR-1998; 10-APR-1997;

15-OCT-1998.

(GEMY) GENETICS INST INC.

Agostino MJ, Jacobs K, Racie LA, Spaulding V, WPI; 1999-070076/06.

Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; hi chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

Homo sapiens WO9845435-A2

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This sequence represents an expressed sequence tag (EST), and is a polymucleotide of the invention. The polymucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, atti-inflammatory activity, adherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 -- CATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 TATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGAACTCATCTCAAGCAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 GIGIACCTIACGCIAIGCIGIGCIIIAGIGGCAICGGCIGCIGGGGGCIIACCIICA---- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 drerangeaakerringedeningraherridegedekedideakededakengreden 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.0%; Score 72; DB 20; Length 520;
Best Local Similarity 51.1%; Pred. No. 1e-10;
Matches 227; Conservative 0; Mismatches 205; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 520 BP; 103 A; 140 C; 123 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 94; 633pp; English.
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652 TGGGCTACATCGTCTTTGACACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGG

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Gaps

. 0

95; Indels

0; Mismatches

248 ATTATATCTGGCACTGCATTGATCTCTTAGATTTCATTACTGTCTTCAGAAAACTCA 189

772 TGATCATCATGTTAAAGAATGCATCTGAGAAGGAAGAAGAAGAA 817

712 ATTACGITAAGCAIGCAIIGACCCITTICACAGAITITIGGCGCIGITTIIGIGGGAIIC 771

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Gaps

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372 293

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RESULT 14 ABQ60318/c

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230 ATTATATCTGGCACTGCATTGATCTTTCTTACATTTCATTACTGTCTTCAGAAAACTCA 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGCTACATCGTCTTTGACACCCCAAGAATTATTGAGAAGGCTCACTTGGGTGATATGG 711
                                                                                                                                                                                                                                                                                                                                                                                                                    TITITIGGIGGIICCAIGGCIGITITCAAGIIIGAGIIGIAITITIGGACICTIGGIGITIG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 TGGGCTTCGTCCTTTTTGATACTCAACTCATTAAAGCCCGAACATGGAGATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 ATTACGITAAGCATGCATTGACCCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATTC
antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                              Query Match
Best Local Similarity 59.3%; Pred. No. 1.3e-09;
Matches 134; Conservative 0; Mismatches 91; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        772 IGAICAICAIGITAAAGAAIGCAICTGAGAAGGAAGAAGAAGAA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 689 BP; 204 A; 157 C; 154 G; 158 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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ABQ58023 standard; cDNA; 506
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Thiaglingam A, Lewis
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                                                                                                                                                                        292
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                                                                                                                                                                                                                                                                       431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 GATCCAAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTGTTTTTTGGTTGCTTCTCA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 akoccekickirociroccacreciriroariesicacesicarieariciriraccieciricace 412
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                                                                   TGGCTTCTCTCAGCTCCTCCTTATCAAGAG -----CAAAAAAAGGGTGGCTCTTCTGATG 371
                                                                                                                                                                        233 rescricarioscial acacercario de la respectación de la respectación
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                                                                                                                                                                                                                                                                             GCAGCTGCACTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTC
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Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGTCTCTCTCTCTGGTTG 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ60318 standard; cDNA; 689
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB7904 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymodeotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primar derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                             Molino GA;
                                                                                       Human colon cancer related nucleotide sequence SEQ ID NO:1718.
                                                                                                                           Human, colon cancer, cancer; tissue profiling, forensic; m
genetic analysis, diagnostic; antisense therapy, gene; ss
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macroarrays on a solid surface, to identify a chromosome on which the
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Sequence 506 BP; 150 A; 100 C; 105 G; 138 T; 13 other;

	l; Gaps 1;	rrgac 671
red. No. 1.7e-07;	Mismatches 85; Indels	612 GTTTTCAAGTTTGAGTTTTTTGGACTCTTGGTGTTTTGTGGCTACATCGTCTTTGAC 671
est Local Similarity 58.3%; Pred. No. 1.7e-07;	atches 120; Conservative 0; Mismatches 85; Indels 1; Gaps	612 GTTTTCAAGTTTGAGTTGTATTTT

²⁸³ ACTCAACTCATTATTGAAAGGCCGAACATGGAGTTCAAGATTATATCTGGCNCTGCATT 224

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⁷³² ACCCTTTTCACAGATTTTGGCGCTGTTTTGTGCGGATTCTGATCATCATGTTAAAGAAT 791 223 GAICTINIINITAGAITICAITACTGINIICAGAAAACTCAIGAIGAINCIGGCCAIGAAT 164 δ

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Search completed: May 25, 2003, 10:14:15 Job time : 290 secs

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304 adchahcacadccaddadacdddanatacciarrrrigddaddarrarigggcrcdddaar 363
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Sequence 1, Appli
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Sequence 44, Appl
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                                                                                                                                                             May 25, 2003, 10:14:23 ; Search time 75 Seconds (without alignments) 4228.050 Million cell updates/sec
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1 gagcaaacataacattgtct.....ataaggaaagttccttgtga 1034
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 17, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 368, Appli Sequence 50, Appli Sequence 20, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli		programmed cell the modification of forestry plant develo	Length 884; Indels 6; Gaps 1;	GOGCTTACCTTCACAT 262 	sgaagcatggtggct 322 		GGCATTAACTTCGATCC 436 	GGTTGCTTCTCAGCTGC 496
18 4 US-09-128-155-17 18 4 US-09-111-470-7 2 US-08-328-254-5 3 US-08-465-293A-1 3 US-08-465-387A-1 3 US-08-463-387A-1 43 4 US-09-102-977-1 43 4 US-09-643-597-368 4 4 US-09-643-597-368 4 4 US-09-453-702B-50 4 4 US-09-453-702B-50 52 3 US-08-947-823-2 52 3 US-08-947-823-2 52 3 US-08-947-823-2 52 3 US-08-947-823-1 53 US-08-947-823-1 54 US-08-768-958-5 55 US-08-768-958-5 64 US-09-268-992-7 65 US-08-768-958-5 66 US-08-768-958-5 67 4 US-09-268-992-7	ALIGNMENTS	. ecting use in ,932A on 3.0	21.4%; Score 221.2; DB 4; 60.6%; Pred. No. 1.4e-52; ive 0; Mismatches 243;	GGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGGTGGGGCTTACCTTCACAT 	CTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTGGTGGCT 	TCTCTGAGCTCCTCCTTATGAAGAGAAAAAGGGTGGCTCTTCTGATGGGAGC 	gcactititgaagggcctctaitggtcctctgattgaggtgggcattaacttcgatcc 	aagcatigtgtinggcgcttttgtaggtigtgctgtggttttggttgcttctcagctgc
28 31.6 3.1 176373 30 31.6 3.1 176373 31 31.2 3.0 692 33 31.2 3.0 692 34 31.2 3.0 692 35 31.2 3.0 692 36 31.2 3.0 692 37 31.2 3.0 692 38 31.2 3.0 692 39 30.8 3.0 2345 41 30.6 3.0 1985 42 30.6 3.0 72604 45 30.6 3.0 72604	E	325-932A-43 ence 43, Applicatic nt No. 6451604 RAL INFORMATION: LICANT: Film, Bay LE OF INVENTION: CE OF INVENTION: CE OF INVENTION: CE REFERENCE: 1022 RENT APPLICATION N RENT APPLICATION N RENT FILING DATE: BER OF SEQ ID NOS: THARE: FastSEQ FOO ID NO 43 NGTH: 884 NGTH: 884 GANLSM: Pinus radi: 325-932A-43	Query Match Best Local Similarity 60. Matches 383; Conservative	203 GGTGTACCTTACGCTA 4 GGTTTATTTGTCGCTT	263 TCTATGGAATATCGGT 64 TCTGTTGAATATTGGA	323 TCTCTCAGCTCCTCCTT	377 TGCACTITTTGAAGGC 184 TGCTGCGTTCAAGGGA	437 AAGCATTGTGTTTGGC
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Pred. No. 1.4e-24;
0; Mismatches 315; Indels
                                                                                                                                                                       APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: A
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MONDTER: IBM PC COMPUT.

OPERATING SYSTEM: PC-DOS/MS-DOS

COFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
ETLING DATE:
CLASSIFICATION: 435
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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NAME: Campbell Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                              Sequence 1, Application US/08818514 Patent No. 5837838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO. 1: SEQUENCE CHARACTERISTICS: LENGTH: 2634 harry
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ilarity 51.9%;
Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La CITY: San Diego STATE: California COUNTRY: United
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Matches 356; Conserv
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TOPOLOGY: lin
US-08-818-514-1
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
SUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ί,
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Pred. No. 4.2e-
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Patent No. 6451604
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, ORGANISM: Pinus radiata
US-09-325-932A-44
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US-09-325-932A-44
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2415 GTCACTCATTTCATTCAGGCTGGCCTGCTGTCTGCCTTGGGCTCCCTGATATTGATGATT 2356
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
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4370 La Jolla Village Drive, Suite 700
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Patent No. 6130317
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1878 dalaagdaraadaagaagaadaa 1853
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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STATE: California
COUNTRY: United States
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US-09-115-934A-1
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        520 GCCCTGAGCTTGTTTGCTTTTGTCCCTGGGGAAT---GTTTTCTTTGGATCCATTTGG 576
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                                                                                                                                                                     577 criticcadacaraccidrateredeaciderideredecarereredecircercrititar 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697 GATCTCTTCTTAGATTCATTACTGTCTTCAGAAACTCATGATGATCCTGGCCATGAAT 756
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                                                                                              612 GTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTGTGGGCTACATCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08818514;
Sequence 2, Application US/08818514;
Patent No. 5837838
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Joila Village Drive, Suite 700
CITY: San Diego
CONTRY: United States
ZIP: 92122
COMPUTER PITT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/818,514
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2446
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792 GCATCTGAGAAGGAAGAAGAAGAA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         757 daaaagaaraagaagaaagaaa 782
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TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 356; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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2295 GGÁTTTGCÁTTCCTTACAGGAATTGGCCTGGGCCCTGCTGCAGTTTTGTATTGCTGTC 2236
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                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                    Length 2634;
                                                                                                                                                                                                               Query Match
11.8%; Score 122; DB 3; Length 26:
Best Local Similarity 51.9%; Pred. No. 1.4e-24;
Matches 356; Conservative 0; Mismatches 315; Indels
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TELEFAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP

Sequence 2, Application US/09115934A Patent No. 6130317

-09-115-934A-2/c

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2535 iridairedecirrrraaaarirrrerdararaacedecreaaeddaedecreaada 2476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.8%; Score 122; DB 3; Length 2634;
Best Local Similarity 51.9%; Pred. No. 1.4e-24;
Matches 356; Conservative 0; Mismatches 315; Indels 1
                                                                                                                                                                                                                        MEDIUM ITER: A TAPEY ALLEAN

COMPUTER: IBM PC COMPAIDLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A

FILING DATE: CLASS: FICKTION DATA:
APPLICATION NUMBER: US 08/818,514

FILING DATE: 14-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: P-LJ 3209

TELECOMMUNICATION INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: P-LJ 3209

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FORCE CHARACTERISTICS:
700
4370 La Jolla Village Drive, Suite
                              CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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US-09-115-934A-2
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1998 ACTCAACTCATTATTGAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCACTGCATT 1939 1938 GATCTCTTCTTAGATTCATTACTGTCTTCAGAAACTCATGATGATGCTGGCCATGAAT 1879 Query Match

4.7%; Score 48.8; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 0.00065;
Matches 14; Conservative 217; Mismatches 159; Indels 0 30472/114 IMMU APPLICATION
FILING DATE: SO AND APPLICATION NUMBER: BP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BANT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (903) 883-4109
TELEFAX: (903) 683-4109
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TURNEY: NUCLEIC ACID CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313 1878 gaaaggaraagaagaagagaa 1853 792 GCATCTGAGAAGGAAGAAGAA 817 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F1s US-08-232-463-14

417 CIGGGCATTAACTTCGATCCAAGCATTGTGTTTTGGCGCCTTTTGTAGGTTGTGCTGTGGTT 476

100 May 4/ 10.40.11 4003

477 ITIGGITGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGG 536

657 TACATCGTCTTTGACACCCAAGAAATTATT 686

597 GGTGGTTCCATGGCTGTTTTCAAGTTTGAGTTGTATTTTGGACTCTTGGTGTTTGTGGGC 656

RESULT 8

WESULT WITH COLUMNING WAS WESULD WESULT STREET STREET

297 GCTTGCATGGGAAGCATGGTGTGGCTTCTCTCAGCTCCTTATCAAGAGCAAAAAGG 356

357 GIGGCICTICIGAIGGCAGCIGCACTITITIGAAGGCGCCTCTATIGGTCCTCTGATIGAG 416

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ercacricarircaricaederidaceierierererecerridaereceierarirarianin 303
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447 TITGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGTTGCTTCTCAGCTGCTGCCAGTTG
                                                                                                                 979 higginaccchichreccchichercchedrichreccmgicecheckericherc
                                                                                                                                                                                                                                                507 GCAAGGCGCAGGAGTACTTGTACCTCGGGGGCCTTCTTTCATCTGGGCGTCTCCTC
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Patent No. 6262334

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: PRODUCTS: II
FILE REPERENCE: CONNA-260XX
CURRENT APPLICATION WHMBER: US/09/386,982
CURRENT APPLICATION NUMBER: 09/328,111
EARLIER PILING DATE: 1999-08-30
EARLIER PILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
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NAME/KEY: misc_feature

LOCATION: (1)...(601)

OTHER INFORMATION: n = A,T,C or G
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Sequence 14, Application US/08981803 Patent No. 6147279 GENERAL INFORMATION:

RESULT 10 US-08-981-803-14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 chdarctraacdrtrangricaarchirrddadddridadagaracddaaarrir 426
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3.3%; Score 34.6; DB 3; Length 2
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109; Indels
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FILE REFERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION WUMBER: PCT/EP96/03052
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1995-07-14
NUMBER: 9514435.8
SAFTIER FILING DATE: 1995-07-14
SERIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE PERENTIN VET. 2.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
3.3%; Score 34.6; DB 3; 1
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109;
                                       INHIBITION OF GENE EXPRESSION
APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHIBITION OF GENE EXPRESS
FILE REPRENCE: 674509-2004
CURRENT PEPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER PILING DATE: 1996-07-12
EARLIER FILING DATE: 1995-07-14
SERLIER FILING DATE: 1995-07-14
SCFTWARE: PATENTING DATE: 1995-07-14
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US-08-981-803-28/C
'Sequence 28, Application US/08981803
'Patent No. 6147279
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-14
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) ORGANISM: Solanum tuberosum
US-08-981-803-28
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DB 4; Length 2169;
  Score 34.6; DB 4; I Pred. No. 3.7; 0; Mismatches 109;
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Batent No. 6232122
GENERAL INFORMATION:
APPLICANT: POULSEN, Peter
TITLE OF INFUNITION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
                                                                                                                                                                                                                                                                                                                                                                                                                             1683 AATAGCTAATGATAGAACATTGACATTTG 1655
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US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
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Best Local Similarity 47.8%;
Matches 100; Conservative
  Query Match
Best Local Similarity 47.8%;
Matches 100; Conservative
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US-08-981-803-29
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US-08-983-440-29
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Best Local
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     1743 GAGTITATGATTAAGTICAATCITAGAATATGAATTTAACATCTATTATAGATGCATAAA 1684
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Patent No. 6232122
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2003
CURRENT FILING DATE: 1998-04-17
BARLIER APPLICATION NUMBER: 9514437.4
BARLIER APPLICATION NUMBER: 9514437.4
BARLIER APPLICATION NUMBER: PCT/EP96/03053
BARLIER APPLICATION NUMBER: PCT/EP96/03053
BARLIER APPLICATION NUMBER: PCT/EP96/03053
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                         APPLICANT POULSEN, Peter
TITLE OF INVENTION; INHIBITION OF GENE EXPRESSION
FILE REPERENCE: 674509-2003
FILE REPERENCE: 674509-2003
CURRENT PELING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER APPLICATION NUMBER: PST/EP96/03053
EARLIER FILING DATE: 1996-07-12
SARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                         1683 AATAGCTAATGATAGAACATTGACATTTG 1655
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                                                                              810 AAGAAGAAGAGAGAGAAACTAGATTTG 838
                                                                                                                                                                                                                                       Sequence 14, Application US/08983440 Patent No. 6232122
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; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-983-440-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-983-440-14
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US-08-983-440-14
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1743 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAACATCTATTATAGATGCATAA 1684
                                                        1863 TATTTTGTTCTCTTATTATTATCATACATTACATTACAAGGAAAGACAAGTACA 1804
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TATTITIGGACTCTTTGTGGGGCTACATCGTCTTTGACACCCCAAGAAATTATTGAG 689
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TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REPERENCE: 674509-2004
CURRENT PELING DATE: 1997-04-17
RABLIER APPLICATION NUMBER: US/08/981,803
CURRENT PILING DATE: 1997-04-17
EARLIER PEPLICATION NUMBER: 9214435.8
EARLIER PILING DATE: 1995-07-14
SARLIER APPLICATION NUMBER: 9514435.8
EARLIER PILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 7.5;
0; Mismatches 109;
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CURRENT FILING DATE: 1998-04-17

EARLIER PEDILCATION NUMBER: 9514437.4

EARLIER FILING DATE: 1995-07-14

EARLIER FILING DATE: 1995-07-12

EARLIER FILING DATE: 1996-07-12

NUMBER: 0F SEQ ID NOS: 35

SOUTHARE: 1996-07-12

SEQ ID NO 29

LENGTH: 11478

CRATURE: NAME/KEY: Variation

LOCATION: (1)..(11478)

OTHER INFORMATION: B stands for G or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: R stands for G or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: R stands for G or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: R stands for G or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: W stands for A or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: W stands for A or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: W stands for A or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: W stands for A or T/U

FEATURE:
NAME/KEY: variation

LOCATION: (1)..(11478)

OTHER INFORMATION: M stands for A or C

US-08-983-440-29
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Query Match 3.3%; Score 34.6; DB 4; Length 11478; Best Local Similarity 47.8%; Pred. No. 7.5; Matches 100; Conservative 0; Mismatches 109; Indels 0;

487 AATAGCTAATGATAGAACATTGACATTTG 51

810 AAGAAGAAGAGAGAGAAACTAGATTTG 838

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Search completed: May 25, 2003, 11:26:51 Job time : 90 secs

us-09-955-526-3.rnpb

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Sequence 22, Appl
Sequence 1827, Ap
Sequence 19, Appl
Sequence 743, Appl
Sequence 356, App
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Sequence 223, Appl
Sequence 17, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 41, Appl
Sequence 41, Appl
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                                                                                                           May 25, 2003, 11:00:18 ; Search time 165 Seconds (without alignments) 8274.897 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US07_NBW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-167-015-33

US-10-167-015-33

US-10-167-015-33

US-10-167-015-3

US-10-219-220-43

US-10-219-220-44

US-10-219-220-44

US-10-167-015-2

US-09-878-574-1827

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Listing first 45 summaries
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ALIGNMENTS

RESULT 1 US-09-955-526-3 Sequence 3, Application US/0995526 Sequence 3, Application US/0995526 Sequence 3, Application US/0995526 Sequence 3, Application US/0995526 SEREAL INFORMATION: TITLE OF INVENTION: of Using Same FILE REFERENCE: P-LJ 4868 TITLE OF INVENTION: of US/09/955.526 CURRENT APPLICATION NUMBER: US/09/955.526 CURRENT FILING DATE: 2000-09-13 PRIOR APPLICATION NUMBER: US/09/661,014 PRIOR APPLICATION NUMBER: US/09/661,014 PRIOR APPLICATION NUMBER: US/09/661,014 PRIOR APPLICATION NUMBER: US/09/661,014 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: UCCATION: (87)(830) NAME/KEY: misc_feature COMMANISH: Lycopersion esculentum FRATURE: NAME/KEY: misc_feature COMMANISH: US/00/04; Pred. NO. 3.2e-313; MANG/KEY: Misc_feature US-09-955-526-3 Query Match Best Local Similarity 100.03; Pred. NO. 3.2e-313; Matches 1034; Conservative 0; Mismatches 0; Indels ON 1 Gaps	1 GAGCAA	QY 61 ACTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAAT 120 Db 61 ACTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCAATTCAATTCGAATTCGAATTCAATTCAATTCGAATTCGAATTCAA	9y 121 CTGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCT 18(
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Publication No. US20030056249A1
GENERAL INFORMATION:
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tac. Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
 TCGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGC
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41.5%; Score 429; DB 9; Length 73
Best Local Similarity 74.5%; Pred. No. 7.1e-124;
Matches 540; Conservative 0; Mismatches 185; Indels
TYPE: DNA
CRGANISM: Glycine max
FEATURE:
NAME/KEY:
LOCATION: (1) ... (735)
US-10-167-015-15
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; Sequence 17. Application US/10167015
; Publication No. US20303056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.; APPLICANT: Johal, Gurmukh
; APPLICANT: Johal, Gurmukh
; APPLICANT: Govedo, Pedro A. Navarro
APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 138
; CURRENT FILING DATE: 2002-06-11
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 17
; LENTH: PASISEQ for Windows Version 3.0
; SEQ ID NO 17
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Pred. No. 3.8e-120;
0; Mismatches 181;
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Best Local Similarity 74.4%;
Matches 526; Conservative (
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, NAME/KEY: CDS

, LOCATION: (37)...(822)

US-10-167-015-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 ATGGTGTGGCTTCTCAGCTCCTCATCAAGAGCAAAAAAGGGTGGCTCTTCTGATG 371
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41.5%; Score 428.8; DB 10; Length 1009;
Best Local Similarity 73.7%; Pred. No. 1e-123;
Matches 560; Conservative 0; Mismatches 197; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Neil
APPLICANT: Hurban, Parith
APPLICANT: Hurban, Parith
APPLICANT: Hurban, Parith
APPLICANTON: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REPREBENCE: 2023US (BARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT PRILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                               Sequence 223, Application US/09770445
Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
                                                                                                                                                                                                                                                                                                                                 Page, Amy
Matthew, Abraham V.
Lefford, Brooke L.
Woessner, Jeffrey P.
Hass, William David
Garcia, Carlos A.
Kricker, Maja
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; ORGANISM: Arabidopsis thaliana
US-09-770-445-223
                                                                                                                                                                                  An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                    Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, Keith R.
Allen, Keith
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APPLICANT:
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             TOGCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACT 429
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                                         CAGCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCTTCTTCAT
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Sequence 31, Application US/10167015

Publication No. US20030056249A1

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tao, Yumán
ITLE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE SEPERENCE: 138
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2001-06-12

PRIOR APPLICATION NUMBER: US 60/297,478

PRIOR PLING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NOS: 34

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SEQ ID NOS: 34
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; LOCATION: (72)...(830)
US-10-167-015-31
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ORGANISM: Zea mays
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US-10-167-015-31
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; Sequence 223, Application US/10219220
; Sequence 224, Application No. US20030082724A1
; Sequence 225, Application No. US20030082724A1
; PUBLICANT: Flinn, Bartin, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; TITLE OF INVENTION: About 100.1022.1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SEQ ID NO 232
; LENGTH: 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                660 ATCGTCTTTGACACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGGATTACGTT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 GITTITGIAGACACTCAAGAAATTATTGAAAGGCCTCACTTTGGTGACCTGGATTATGTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 AAGCAIGCAITGACCCITITICACAGAITITIGGCGCTGITITIGIGCGGAITCIGAICAIC 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 AAGCATGCATTGATTGTTCACTGATTTGGCTGCAATCTTTGTGCGAATTCTTATATA 726
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                                                                                                        367 derairiseceairganeenageeninairginagraearirisisesaasineiningeeniin 426
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                                                                                                                                                                                  427 GCTTGCTTCTCTGCGGCAGCTTTAGTTGCAAGGCGTAGGGAGTACCTCTACCTTGGTGGT 486
                                                                                                                                                                                                                                         540 CTTCTTTCATCTGGCGTCTCCCTTCTCTTGGTTGCACTTTGCATCCTCCATTTTTGGT 599
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420 GGCATTAACTTCGATCCAAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 ATGTTAAAGAATGCATCTGAGAAGGAAGAAGAAGAAGAAGAAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
, ORGANISM: Eucalyptus grandis
US-10-219-220-232
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Matches 519; Conservat
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| Publication No. US20030056249A1
| GENERAL INFORMATION:
| APPLICANT: Simonons, Carl R.
| APPLICANT: Simonons, Carl R.
| APPLICANT: Gordon-Kamm, William J.
| APPLICANT: Johal, Gurmukh
| APPLICANT: Accepted, Pedro A. Navarro
| APPLICANT: Accepted, Pedro A. Navarro
| APPLICANT: Accepted, Pedro A. Navarro
| TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
| TITLE OF INVENTION: Thereof
| TITLE OF INVENTION: Thereof
| TITLE OF INVENTION: Thereof
| TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
| TITLE OF INVENTION NUMBER: US/10/167,015
| CURRENT APPLICATION NUMBER: US 60/297,478
| PRIOR FILING DATE: 2001-06-12
| PRIOR FILING DATE: 2001-06-12
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
APPLICANT: Johal, Gurmukh
APPLICANT: Tao, Yumin
TITLE OF INVENTION: Thereof
FILE REFERENCE: 1388
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ 1D NOS: 34
SOFTWARE: PASLEGO for Windows Version 3.0
SEQ 1D NO 33
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886 AAGAGGAGGAAGAGGA 901
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US-10-167-015-5
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Publication No. US20030056249A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Johal, Gurmush
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tao, Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
                                                                                                                                                                      Query Match 30.0%; Score 310.4; DB 9; Length Best Local Similarity 64.8%; Pred. No. 1.5e-86; Matches 477; Conservative 0; Mismatches 256; Indels
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30.0%; Score 310.4; DB 9; Length 1139;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256; Indels 3;
FILE OF INVENTION: Thereof
FILE REFERENCE: 138
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
FRICOR APPLICATION NUMBER: US 60/297,478
FRICK FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FREESEQ for Windows Version 3.0
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APPLICANT: Gorden-Kamm, William J.
APPLICANT: Gorden-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Acevedo, Pedro A. Navarro
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
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Pred. No. 6.9e-85;
0; Mismatches 235; Indels
                                                                                                       Sequence 3, Application US/10167015
Publication No. US20030056249A1
GENERAL INFORMATION:
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TILE OF INVENTION: death and their use in the modification of plant development
TILE OF INVENTION: 022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NO 231
LENGTH: 1102
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23.8%; Score 245.6; DB 9; Length
Best Local Similarity 60.6%; Pred. No. 3.1e-66;
Matches 423; Conservative 0; Mismatches 269; Indels
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737 TITCACAGAITITIGGCGCTGITITIGTGCGGAITICTGAICATCATGTTAAAGAAIGCAIC 796
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                                                                                                                                                                                                                                                   604 CAGTAATTCCAGGGAAGGGAAAAAAAAGAAGAA 635
                                                                                                                                                                       797 TGAGAAGGAAGAAGAAGAAGAAGAGAGAA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 CAGCTGCTGCCATGTTGGCAAGGCGCAG 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 44, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
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Publication No. US20030056249A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-44
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-219-220-44
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Publication No. US20030082724A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: 1000-102ca1
CURRENT PALICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER: OF SEQ ID NOS: 290
SOSTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617 CAAGITIGAGITGIATITIGGACICTIGGIGITIGIGGGCIACAICGICTITGACACCCA 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACTITITGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGGCATTAACTTCGATCC 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 GGIGIACCTIACGCIAIGCIGIGCTITIAGIGGCAICGGCIGCIGGGGCTIACCTITAACAT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 criariccercéracirecresascaarsasestaas de criaces de cria consecret de consecret
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                                                                                                                                                     694 CACACAGATGATCATCGAGAAAGCGGACCATGGAGACTATGATTATTAAAACATTCACT 753
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21.4%; Score 221.2; DB 9; Length 8
Best Local Similarity 60.6%; Pred. No. 1.2e-58;
Matches 383; Conservative 0; Mismatches 243; Indels
                                                                                                                                                                                                                                                                 791 TGCATCTGAGAAGGAAGAAGAAGAAGAAGAGGAGAA 828
                                                                                                                                                                                                                                                                                                                                         814 TGCAGACAGTAAATCCAGGGAAGGGAAAAAGAAGAGAA 851
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ORGANISM: Pinus radiata
US-10-219-220-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-219-220-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 43
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APPLICANT: Film, Barry
APPLICANT: Film, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Geath and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT PILING DATE: 2002-08-14
FIRING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NOS: 290
SEQ ID NO 44
LENGTH: 527
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; Publication No. US20030056249A1
; GENERAL INPORMATION:
APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
APPLICANT: Johal, Gurmukh
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 138
CURRENT APPLICANTON WHBER: US/10/167,015
; CURRENT PILING DATE: 2002-06-11
; PRIOR FILING DATE: 2001-06-12
APPLICANT: Tao, Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: 1386
CURRENT APPLICATION NUMBER: US/10/167,015
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 740
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Pred. No. 2.1e-45;
0; Mismatches 152;
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Similarity 64.0%;
70; Conservative (
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; LOCATION: (64)...(489)
US-10-167-015-7
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ORGANISM: zea mays
FEATURE:
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Matches 270; (
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US-10-167-015-22
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                                                                                                                                                                                                                                                                                                                          Length 308;
                                                                                                                                                                                                                                                                                                                             Query Match 17.2%; Score 177.8; DB 9; Length Best Local Similarity 75.6%; Pred. No. 2.4e-45; Matches 232; Conservative 0; Mismatches 74; Indels
NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 22

LENGTH: 308

TYPE: DNA
ORGANISM: glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (308)

COTHER INFORMATION: n = A,T,C or G
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750 bp mRNA linear EST 31-JAN-2001
CTOF4L8 5' sequence, mRNA sequence.
BG124317
EG124317.1 GI:12624505
BG134507 EST467399
BG115430 EST560993
BF054243 EST560993
BF05537 EST564820
BG115431 EST564820
BG115431 EST564820
BG115431 EST56441
AM739750 EST310250
BE919556 EST310250
BM932823 EST3158666
AM932823 EST3158666
AM939749 EST310249
BG91270 GGF22G16.
BG64692 EST510249
BG965331 GGEZD6.
BG646972 EST510249
BG646972 EST510331
BG725427 MTWAG62TK
BE577220 L48-2040T
BG792694 EST 8414
BG77198 BNLGH1671
A172198 BNLGH1671
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A1731928 BNLGH167314
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BQ246217 TaE15014G
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AW329256 N200474e
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
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1 (bases 1 to 750)

van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTE from tomato shoot/meristem tissue
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemeor University Genomics Institute
Clemson University
100 Tordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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Coganism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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BG648573
BG647209
BQ647209
BQ401834
BQ105367
AI72083
AI726851
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BG124317
LOCUS
DEFINITION
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VERSION
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AUTHORS
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B1933489 EST553378
AN096641 EST289821
AN219279 EST391761
BG127849 EST49155
A1779122 EST260001
                                                                                                                 May 25, 2003, 09:52:48 ; Search time 1487 Seconds (without alignments) 11261.690 Million cell updates/sec
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                        GenCore version 5.1.5
(c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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/tissue_type="shoot/meristem"
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Xho1; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
a 174 c 176 g 242 t
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/note="Vector: pBluescript Site_2: The
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bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
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/organism="Lycopersicon er/
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/db xref="taxon:4081"
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/cultivar="mio Grande PtoR"
/dultivar="mio Grande PtoR"
/done="clET39M"
/clone="clET39M"
/clone="clET39M"
/clone=lib="tomato mixed elicitor, BTI"
/clone=lib="tomato mixed elicitor, BTI"
/dev stage="4-6" week old plants"
/dev stage="4-6" week old plants"
/lab_host="XLI-Blue MRP""
/lab_host="XLI-Blue MRP""
/note="vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
/note="vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
/note="vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
/note="vector: pBlueScript of disease response
elicitors: Plants exposed to 2,6 dichloroisonicotinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."
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1 (Dases 1 to 643)

1 (Ascenzo, M., He.X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,

1 Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,

Reser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                  EST289821 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET39M7, mRNA sequence.
AW096641
AW096641.1 GI:6062236
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                                                                                                                                   GGCGICTCCCTTCTCTTCTGGTTGCACTTTGCATCCTCCATTTTTGGT-GTTCCAGGCT
 GATCCAAGCATTGTGTTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTTGGGTTGCTTCTCA
                         481 Gerecrecarerrescaagececaceastreractreraceresceretrirearer
                                                        GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGGCCCTTCTTTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deneration of ESTs from tomato leaf tissue Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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llarity 100.0%; Pred. No. 3.8e-154;
Conservative 0; Mismatches 0;
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Best Local Simi
Matches 643;
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GCAAACATAACATIGICTACGTICAGATAAATAICCITIGCICATTICAGTICCAAAAÀC 62

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AW219279 646 bp mRNA linear EST 18-MAY-2001 EST201761 tomato root during/after fruit set, Cornell University Lycopersicon esculentum cDNA clone cLEX3N8, mRNA sequence. AW219279
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van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato root tissue
Unpublished (1999)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Unpublished (2001)
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BG127849 1 G1:12628037
EST.
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/db xref="taxon:4081"
/clone="clastne"
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/dev.stage="clastne"
/dev.stage
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61.3%; Score 634; DB 10; Length 640
Best Local Similarity 99.8%; Pred. No. 7.8e-152;
Matches 645; Conservative 0; Mismatches 0; Indels
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/dev_stage="developing shoots from 4-6wks old plants"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="voctor: pBluescript SK(-); Site_1: EcoR1; Site_2:
Xho1; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
99 a 154 c 153 g 211 t
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                             1. (bases 1 to 647)
and der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utt
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
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Contact: CUGI
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                                                                    596 bp mRNA linear EST 18-WAY-2001 clone CLES7M13, mRNA sequence.
A1779122 A1779122.1 GL:5277163
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                      D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B. Generation of ESTs from Pseudomonas susceptible tomato Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 TGGTCCTCTGATTGAGCTGGGCATTAACTTCGATCCAAGCATTGTGTTTGGCGCTTTTGT 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTGTGTGGCTTCTCTCAGCTCCTCCTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 TCAAGAGCAAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACTTTTTGAAGGCGCCTCTAT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 CTTCCGCCAGAICTCACCTCTCGTTCAAACTCATCAAGGAGGTGTACCTTACGCTATG 220
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/organism="Lycopersicon esculentum"
/oultivar="Rll-13 (Rio Grande x Money Maker)"
/dD xref="taxon:4081"
/clone="cles7M13"
/clone lib="tomato susceptible, Cornell"
/tissue_type="leaf"
/dev stage="4-week old"
/lab_host="SOLR"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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100.0%; Pred. No. 4.3e-142;
tive 0; Mismatches 0; Indels
 647
                                  647
                     601 TTCCATGGGCTGTTTTCAAGTTTGAAGTTGTATTTTGGACTCTTGGTG
GTTCCATGGCTGTTTTCAAGTTGAGTTGTATT
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Matches 596; Conservative
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                                                                                    RESULT 6
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592 bp mRNA linear EST 31-JAN-2001
EST467399 tomato crown gall Lycopersicon esculentum cDNA clone
CTOEL6F5 5' sequence, mRNA sequence.
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/dev_stage="crown galls from full-grown plants (8 wks old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
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                                                                                                            GTACTIGITACCTCGGGGGCCTTCTTTCATCTGGCGTCTCCCTTCTCTTTTGCACTT
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                                                                GTACTTGTACCTCGGGGGCCTTCTTTCATCTGGCGTCTCCCTTCTTCTGGTTGCACTT
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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van der Hoeven, S., Sun, H., Cho, J., Utterback, T.,
C. and Tanksley, S.
Generation of ESTs from tomato crown gall tissue
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|db xref="taxon:4081"
|clone="crosi6Fs"
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/tissue type="crown gall"
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BF054243 EST439473 potato leaves and petioles Solanum tuberosum cDNA clone eST339473 potato leaves and petioles Solanum tuberosum cDNA clone eST339421 5' sequence, mRNA sequence.
BF054243.1 GI:10808139
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I, (bases I to 540)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Unpublished (2000)
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tubers, or roots."

140 c 137 g 184 t
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                                                                                                                                                                                     51.7%; Score 534.2; DB 14; Length 578; 96.5%; Pred. No. 3e-126; Live 0; Mismatches 18; Indels 2;
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Matches 557; Conservative
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Solanum:
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum:
E 1 (Bases II to 578)
Subell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20167379.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYLLD43U STR DOLATO 578 bp mRNA linear EST 22-JUL-2002 EST600993 mixed potato tissues Solanum tuberosum cDNA clone STMDA93 5' end, mRNA sequence. BQ115430 BQ115430.2 GI:21916950 EST.
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This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAACTTCGATCCAAGCATTGTGTTTGGCGCTTTTGTAGGTTGTGCTGTGGTTTTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCT
                                                                                                                                                                                                      TCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCT
                                                                                  123 GCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCAACTTC
                                                                                                                                121 eccreteccaaccecresagriarearicaicaaaaacricesceasarcreacter
                                                                                                                                                                              GITCAAACTCATCTCAAGCAGGTGTACCTTTACGCTATGCTGTGCTTTAGTGGCATCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTCATCTGGCGTCTCCCTTCTTTCTGGTTGCACTTTGCATCCTCCATTT 594
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1. 578
/ Organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMDA93"
/clone lib="mixed potato tissues"
/tissue_type="mixed tissues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cdna@resgen.com
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RESULT 8 BQ115430 LOCUS DEFINITION

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543

541

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

430

250 241

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Lycopersicon esculentum
Sukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="flower"
/dev stage="anthesis"
/dev stage="anthesis"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xhol; Supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                  1 (bases 1 to 476)
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                         Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recercicecaaccecreaagirarearicicicaaaacriceccaearcreacter 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AGCAAACATAACATTGTCTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAAA
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                                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Bmail: http://www.genome.clemson.edu/orders/index.html
lis clone is available through the Clemson University
Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="tomato flower, anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum"
/cultivaz="TA496"
/db_xref="taxon:4081"
/clone="cTOD22C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.3%; Score 468.8; DB 13; 99.6%; Pred. No. 1.7e-109; tive 0; Mismatches 2;
                                                                                                                                                                                                                                                           Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 470; Conservative
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                                                                                                                                                                                                                                                                                                                      /note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B1935239 476 bp mRNA linear EST 18-OCT-2001 EST55128 tomato flower, anthesis Lycopersicon esculentum CDNA clone cTOD22C8 5' end, mRNA sequence.
B1935239.1 G1:16249711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 GAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 Traccricacarrerandeaararegregecrecreacaacarregerrecaregaag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 CGATCCAAGCATTGTGTTTGGCGCTTTTTGTAGGTTGTGCTGTGGTTTTTTGGTTGCTTCTC 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                     Libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 540;
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                1.540
/organism="Solanum tuberosum"
/cultivax="Kennebec"
/cultivax="taxon:4113"
/clone="cSTB39K21"
/clone lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 498.4; DB 12; Length
Pred. No. 4.5e-117;
0; Mismatches 16; Indels
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Matches 521; Conservative
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                                                                                                                                                                    RESULT 12
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422
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                  A18953/7
EST254820 tomato callus, TAMU Lycopersicon esculentum cDNA clone at 22C7119, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloue libe trong callus, TAMU"

/tissue type="callus"

/tissue type="callus"

/dev_stage="25-40 dmRF""

/lab_host="XL-Blue MRF""

/note="Vector: pBlueScript SK(-); Site_I: EcoRI; Site_2:

Xhoi; supplier: Giovannoni laboratory; CLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.

Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

a 112 c 116 g 137 t
                                                                                                                                                                                                                                                        Lycopersicon.

1 (bases 1 to 464)

1 (bases 1 to 464)

1 (bases 2 to 464)

Liang, F., Upton, J., Krabalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato callus tissue
Unpublished (1999)
                                                                                                                                                                             Lycopersicon esculentum
Eukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TCTTCTGATGGCAGCTGCACTTTTTGAAGGCGCCTCTATTGGTCCTCTGATTGAGCTGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CATGGGAAGCATGGTGGCTTCTCTCTCTCTCTCTTCTTCAAGAGAAAAAAGGGTGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCCACCTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 IGCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CAIGGGAAGCAIGGIGIGGCIICTCICAGCICCTICTIAICAAGAGCAAAAAGGGIGGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TECTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCCTCACAACAATGGCTTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGAAGAAGAAGAAGAAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTCGAAGAAGAAGAAGAAGATCAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATC 60
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Best Local Similarity 98.7%; Pred. No. 8.3e-106;
Matches 458; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
| volitiva="TA46"
| db xref="taxon:4081"
| clone="cLEC7H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prime sequence.
Location/Qualifiers
                                                                                                                  AI895377.1 GI:5601279
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                                                          DEFINITION
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JOURNAL
COMMENT
      RESULT 11
AI895377
LOCUS
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AUTHORS
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Location/Qualifiers

Location/Qualifiers

1. 617

/organism="Solanum tuberosum"

/oultvar="Rannebec or Binjte"

/db xref="maxon.4113"

/clone="STMDA93"

/clone="STMDA93"

/clone="STMDA93"

/lab_host="SolR"

/lab_host="Yeacor: pBluescript SK(-); Site_1: EcoRI; Site_2:

/note="Vector: pBluescript SK(-); Site_1: Site_2:

/note="Vector: pBluescript of untreated and Phytophinora

infestans-treated libraries of stolons, leaves, leaflets,

axillary buds of stem explants, petioles, germinating eyes

, tubers, or zoots.

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This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or chaeresgen.com
Seq primer: 17.
                                                                                                                                                                                                                                                                                                                                                            p mRNA linear EST 17-APR-2002
Solanum tuberosum cDNA clone STMDA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum

Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots,
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (Dases I to 617)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Garamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557 Addingigenegininingeniecnichadenecheckandingekadedenagea 498
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481
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                                      361 CATTAACTTCGATCCAAGCATTGTGTTTGGCGCTTTTGTAAGTTGGGCTGTGGTTATTG
CATTAACTTCGATCCAAGCATTGTGTTTTGGCGCTTTTTGTAGGTTGTGCTGTGGTTTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onpunistry (2018)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                  525
                                                                                                                                                                                             421 Triccrictaecracracrascaratrasca addeca addecrata 464
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43.4%, Score 449.2; DB 14;
Best Local Similarity 89.9%; Pred. No. 1.9e-104;
Matches 524; Conservative 0; Mismatches 34;
                                                                                                                              482 TIGCITCICAGCIGCCAIGITGGCAAGGCGCAGGAGIACI
                                                                                                                                                                                                                                                                                                                                                            617 bp
ESTG00994 mixed potato tissues S
3' end, mENA sequence.
BQ115431
EQ115431.1 GI:20167380
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RESULT 14
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/ organism="Livropersion esculentum"
/ do_xref="taxon:4081"
/ do_xref="taxon:4081"
/ do_xref="taxon:4081"
/ do_e="classus.188"
/ clone lib="tomato resistant, Cornell"
/ tissue_type="leaf"
/ dab_host="sola"
/ lab_host="sola"
/ hote="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhoi, class - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-)
) at 5, end with EcoR1 and 3, end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                   AI776541 Homato resistant, Cornell Lycopersicon esculentum CDNA clone CLER18J18, mRNA sequence.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
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D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Frasch, Wenter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 456; 1988, 1898, 1898
                                                                                                                    197 GAGGAGAAACTAGATTTGGTTCTATGGGCTACTGGGACTCTAACCTGTGTGGTTTTCATA 138
   377 cridendrindrescracarnercrineacacccaasaarrarreadaadecreacri 318
                                                                                                    TGTGCGGATTCTGATCATCATGTTAAAGAATGCATCTGAGAAGAAGAAGAAGAAGAAGAA 820
                                                                                                                                                                    861
                                                                                                                                                                                                                                      862 ACTCCTTGTGTTCACCTGAAACAAGCATGTTAATAGTTTGATACTTGCTTCACTTTAGCA 921
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                                                                                                                                                                    GAGGAGAAACTAGATTTGCTTCT--------CAACTTGTGGTTTCCANA
                                                                                                                                                                                                                                                         137 ATACACTGTGTTCACCTGAAACAAGCATGTTAATAGTTTGAAACTAG-----CTTTAGCA
                                                          GGGTGATATGGATTACGTTAAGCATGCATTGACCCTTTTCACAGATTTTGGCGCTGTTTT
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 1.5e-101;
0; Mismatches 2;
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AI776541.1 GI:5274582
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Best Local Similarity 99.3%;
Matches 450; Conservative (
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Contact: CUGI
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
DEFINITION
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JOURNAL
COMMENT
                                                                                                    761
                                                                                                                                                                      821
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
AI776541
                                     701
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EST310250 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT8N10 5', mRNA sequence.
AW399750
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Lycopersicon pennellii
Eukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,J.E.
Liang,F., Hansen,T.S., Upcon,J., Roming,C.M., Craven,M.B., Fujii
,C.Y., Bowman,C.L., Nierman,W., Fassr,C.M., Venter,J.C., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
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/db xref="taxon:28526"
/clone="clpT8N10"
/clone lib="lb: pennellii trichome, Cornell University"
/tissue_type="trichome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid
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78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 CACTITITGAAGGCGCCCTCTAITGGCCCCTCTGAITGAGCTGGGCAITAACTICGAICCA
                                                                                                                                                                                                                          GGAGTTATGATTCTCTCAAAAACTTCCGCCAGATCTCACCTCTCGTTCAAACTCATCTCA
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                                      CTACGTTCAGATAAATATCCTTTTGCTCTTTTTCAGTTCCAAAAACTCGAAGAAGAAGAAGA
                                                                                                                                               AGAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               259 ACATICIATGGAATATCGGTGGCCTCCTCACAACAATGGCTTGCATGGGAAGCATGGTGT
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CTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAAACTCGAAGAAGAAGAAGA
                                                                                                        AGAGAACAATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCT
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 AGCATTGTGTTTGGCCCTTTTGTAGGTTGTGCT 470
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/lab_host="SOLR"
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Unpublished (1999)
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nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
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(bases 1 to 488)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Verterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tankeley, S.D. and Baker, B.
Generation of ESTS from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 bp mRNA linear EST 02-OCT-200
EST423325 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB1D22 5' sequence, mRNA sequence.
EB919556
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                                                                                                                                                                     TAACATTGTCTACGTTCAGATAAATATCCTTTGCTCATTTCAGTTCCAAAAACTCGAAGA 69
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                                                                                                   Length 448;
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The Institute for Genomic Research
For clone request: please contact Research Genetics
Division tel 1.800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                    15, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_vare="taxon:4113"
/clone="cSTB1D22"
/clone_lib="potato leaves and petioles"
                                                                                                   Score 423; DB 10;
Pred. No. 9.3e-98;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 TCGATCCAAGCATTGTGTTTGGCGCTT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGATCCAAGCATTGTGTTTGGCGCTT 448
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                                                                                                     tch 40.9%; al Similarity 96.6%; 432; Conservative
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Best Local S:
Matches 432
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VERSION
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                                                                            /note="Vector: pBlueScript SK(-), Site 1: EcoR1, Site 2: Xho1, Tissue was supplied by Dr. Fry (Cornell University) Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
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ო
                                                                                                                                                                                                                                                                                                                                                     Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                               25; Indels
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                     Query Match 40.8%; Score 422; DB 12; Best Local Similarity 94.1%; Pred. No. 1.7e-97; Matches 450; Conservative 0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 25, 2003, 11:25:15 Job time : 1494 secs
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May 25, 2003, 11:25:24 ; Search time 62 Seconds (without alignments) 533.002 Million cell updates/sec
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1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                         908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                             US-09-955-526-4
                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                               Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Testis Enhanced Ge	Testis Enhanced Ge	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Bovine mammary tis	Lung cancer associ	Bax inhibitor BI-1	Human ovarian anti
	ID	AAB65755	AAB65756	AAG19970	AAG19969	AAG19971	AAG54829	AAB87615	AAB58178	AAW73136	ABP42996
		22	22	21	21	21	21	22	21	19	23
	Query Match Length DB	213	140	138	154	110	129	236	255	237	245
dю	Query	54.1	39.3	39.2	39.5	38.9	38.7	38.6	38.0	37.5	26.1
	Score	688.5	499.5	498.5	498.5	495	492.5	491.5	483.5	477.5	331.5
	Result No.		8	· "	। ধা	S	9	7	80	σ	10

Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in

Novel human secret	hila.	Ë	-	n adi	Human secreted pro	ted	tes	Human haemopoietic	Membrane-bound pro	Human DERP2 protei	Human PRO281 (UNQ2	Human polypeptide	Human Pro peptide	Human polypeptide	Human secreted pro	4	cancer a	Gene 16 human secr	Human TPAAAG12 pol	<u>.</u>	ñ	rosophi	Ä	rosophi	ea mays	ea mays protein	ecreted protein	protein	s thali	is thali	s thali	neurotrans		Hindan ORF1966
8 LCOFII A	ABB63069	00	-	31	~	49	99	AAY79139	AAY66631	43	AAB65154	ABP61812	ABG34030	ABB89838		AAY76620	AAB43975	AAB64489	AAY83263	731	AAG33365	318	AAG33367	019	AAG33366	72	AAY59658	AAG44723	20	AAG52200	AAG52199	AAY77122	AAM93503	AAB42202
00	3 6	22	22	21	21	22	20	21	2	21	22	23	23	23	19	20	21	22	21	50	21	22	21	22	21	21	20	21	21	21	21	21	22	21
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ALIGNMENTS

Cell death modulator; programmed cell death; PCD; apoptosis; Testis Enhanced Gene Transcript protein #1. (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD. AAB65755 standard; Protein; 213 AA 02-JUN-2000; 2000WO-NZ00086. 99US-0325932. 27-MAR-2001 (first entry) WPI; 2001-061724/07. N-PSDB; AAF44782. Flinn B, Lasham A; WO200075331-A1. forestry plant. Pinus radiata. 04-JUN-1999; 14-DEC-2000. AAB65755; AAB65755

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AAG19970;
                                                                                      Sequence
                                                                                                          Query Match
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                                     The present invention relates to coding sequences (see AAF44740-F44840 prod AAF4443-F44844) and proteins (see AAB65714-B65614) involved in programmed cell death (PCD; apotrosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in
                                                                                                                                                                                                                                         61 AAAFKGATLGPLIDAVINIDSSILVSAFVGTSLAFACFSAAAITARRREYLFLGGLLGSG 120
                                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                     157 VSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALT 216
                                                                                                                                                                     Gaps
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                                                                                                                                                                                        39 QVYLTLCCALVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSAP--PYQEQKRVALLMA 96
                                                                                                                                                                                                    97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSG
                                                                                                                                                                     3;
                                                                                                                                                Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell death modulator; programmed cell death; PCD; apoptosis;
                                                                                                                                                                     41; Indels
                                                                                                                                               54.1%; Score 688.5; DB 22;
64.6%; Pred. No. 3.8e-73;
ive 31; Mismatches 41; I
                                                                                                                                                                                                                                                                                                                                                                                                                                             Testis Enhanced Gene Transcript protein #2.
                                                                                                                                                                                                                                                                                                              LFTDFGAVFVRILLIMLKNA-SEKEEKKKKRR 247
                                                                                                                                                                                                                                                                                                                                212
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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                     Claim 22; Pages 81-82; 142pp; English.
                                                                                                                                                                                                                                                                                                                               LFIDFVAVFVRLMVIMAKNADSKSREGKKKRR
                                                                                                                                                                                                                                                                                                                                                                                   AAB65756 standard; Protein; 140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                             Best Local Similarity ox.v. Matches 137; Conservative
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                                                                                                                                213 AA;
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   forestry plant
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                                                                                                                                Sequence
                                                                                                                                                   Query Match
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The present invention relates to coding sequences (see AAF44740-F44840 and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD, apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEGETSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL
                                                                                                                                                                                                                                                                                           39.3%; Score 499.5; DB 22; Length 140; 66.2%; Pred. No. 5.8e-51; ive 14; Mismatches 26; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 21975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FGAFVGCAVVFGCFSAAAMLARREYLYLGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ISAFVGSALAFACFSGAA-----CWLGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG19970 standard; Protein; 138 AA
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
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99US-0132863.
99US-0134256.
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99US-0129845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                   Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                 140 AA;
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01-APR-1999
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23-APR-1999;
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99US-0134219. 99US-0134219. 99US-0134211. 99US-0134721. 99US-01347841. 99US-0135353. 99US-0135353. 99US-0135353. 99US-0135352. 99US-0136392. 99US-0136392. 99US-0137522. 99US-0137528. 99US-0137528. 99US-0137528. 99US-0137528. 99US-0139453. 99US-0140353. 99US-0140353. 99US-0140353. 99US-0140353. 99US-014287.	910S - 0143542 910S - 0144062 910S - 014408 910S - 014408 910S - 0144333 910S - 0144333 910S - 0144333 910S - 0144333 910S - 0144333 910S - 0144633 910S - 014508 910S - 014508
14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 18-MAY-1999; 20-MAY-1999; 20-MAY-1999; 22-MAY-1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-UNN-1999; 26-UNN-1999; 26-UNN-1999; 26-UNN-1999; 26-UNN-1999; 26-UNN-1999; 27-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 28-UNN-1999; 29-UNN-1999; 29-UNN-1999; 29-UNN-1999; 29-UNN-1999; 29-UNN-1999; 20-UNL-1999; 20-UNL-1999; 20-UNL-1999; 20-UNL-1999; 20-UNL-1999; 20-UNL-1999;	
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PR 23-JUL-1999; 99US-0145224.

PR 27-JUL-1999; 99US-0145218.

PR 27-JUL-1999; 99US-0145518.

PR 27-JUL-1999; 99US-0145518.

PR 27-JUL-1999; 99US-0145518.

PR 28-JUL-1999; 99US-0145518.

PR 28-JUL-1999; 99US-0145518.

PR 02-AUG-1999; 99US-0147204.

PR 02-AUG-1999; 99US-0147204.

PR 02-AUG-1999; 99US-0147204.

PR 02-AUG-1999; 99US-0147204.

PR 03-AUG-1999; 99US-0147204.

PR 12-AUG-1999; 99US-0147204.

PR 12-AUG-1999; 99US-0147204.

PR 13-AUG-1999; 99US-0147204.

PR 13-AUG-1999; 99US-0147204.

PR 13-AUG-1999; 99US-014936.

PR 13-AUG-1999; 99US-014936.

PR 13-AUG-1999; 99US-014936.

PR 22-AUG-1999; 99US-014936.

PR 22-AUG-1999; 99US-014936.

PR 22-AUG-1999; 99US-014936.

PR 23-AUG-1999; 99US-014936.

PR 23-AUG-1999; 99US-0151065.

PR 24-AUG-1999; 99US-0151065.

PR 25-AUG-1999; 99US-0151065.

PR 25-A

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99US-0134256
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                                                                                                                                                                                                                                             1 MEGFISFEDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                             Query Match

39.2%; Score 498.5; DB 21; Length 138;
Best Local Similarity 70.5%; Pred. No. 7.5e-51;
Matches 91; Conservative 21; Mismatches 16; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG19969 standard; Protein; 154 AA.
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990S-0123180.
990S-0125788.
990S-0125788.
990S-0126264.
990S-0127465.
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990S-0127465.
990S-0127465.
990S-0130891.
990S-0131449.
990S-0132486.
990S-0132486.
99US-0160989.
99US-0161404.
99US-0161406.
99US-0161359.
99US-0161350.
99US-0161360.
99US-0161920.
99US-0161992.
99US-0161993.
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22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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19-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
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06-MAY-1999;
07-MAY-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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AAG19969

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990S-0144325.
990S-0144331.
990S-0144332.
990S-0144333.
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99US-0144352.
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99US-0145088.
99US-0145085.
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99US-0145192.
99US-0145145.
99US-0134218.
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PR 23-VUL-1999; 99US-0145218.

PR 23-VUL-1999; 99US-0145224.

PR 27-VUL-1999; 99US-0145224.

PR 27-VUL-1999; 99US-0145219.

PR 27-VUL-1999; 99US-0145211.

PR 27-VUL-1999; 99US-0145211.

PR 02-AUG-1999; 99US-0145211.

PR 02-AUG-1999; 99US-0147028.

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PR 11-AUG-1999; 99US-014864.

PR 11-AUG-1999; 99US-014864.

PR 12-AUG-1999; 99US-014864.

PR 12-AUG-1999; 99US-014864.

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PR 22-AUG-1999; 99US-014864.

PR 22-AUG-1999; 99US-014866.

PR 23-AUG-1999; 99US-014806.

PR 23-AUG-1999; 99US-015906.

PR 23-CCT-1999; 99US-0159
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                                                                                                                                                  1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                            DB 21; Length 154;
                                                                                                                Match 39.2%; Score 498.5; DB 21; Length Local Similarity 70.5%; Pred. No. 8.6e-51; Local Similarity 21; Mismatches 16; Indels
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PR 27-UUL-1999; 99US-0145219.

PR 27-UUL-1999; 99US-0145319.

PR 02-MUG-1999; 99US-0145319.

PR 02-MUG-1999; 99US-014726.

PR 02-MUG-1999; 99US-014726.

PR 02-MUG-1999; 99US-014732.

PR 03-MUG-1999; 99US-014732.

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PR 13-MUG-1999; 99US-014772.

PR 13-MUG-1999; 99US-0151080.

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                                                                                                                                                                                    139 MLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQE 198
                                                                                                                                                                 Gaps
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                                                                                                                                                                5; Indels
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                                                                                                                                            Query Match
38.9%; Score 495; DB 21;
Best Local Similarity 86.4%; Pred. No. 1.4e-50;
Matches 95; Conservative 10; Mismatches 5;
                                                                                                                                                                                                                                                                                                    AAG54829 standard; Protein; 129 AA
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New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells -
                                                                                                                                                                                                                                                              60 WNIGGILTTIGCIGTMIWLLSCPPYEHQKRLSLLFASAVLEGASVGPLIKVAIDVDPSIL 119
                                                                                                                                                                                                                                               WNIGGLLTTMACMGSWWILLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                           1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHIL 60
                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                            The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting the angiogenesis and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                           DB 21; Length 129;
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Local Similarity 71.4%; Score 492.5; DB 21; Length
Local Similarity 71.4%; Pred. No. 3.5e-50;
Les 90; Conservative 20; Mismatches 15; Indels
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(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine mammary tissue derived protein #6.
                                                                                                                                                                                                                                                                                                                                                                                              AAB87615 standard; protein; 236 AA.
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99US-0161404.
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99US-0161361.
99US-0161920.
99US-0161932.
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                                                                                                                                                                                                                                                                                                                                                                                 Human, lung cancer associated protein; neuroprotective, cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polymucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and general; unmunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide sequences. The lung cancer associated chromosome identification, as chromosome markers, and for numerous othromosome identification, as chromosome markers, and for numerous chromosome ic an exact purposes. The proteins may be used to treat disporders such as neural; immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                       187
                                                                                                             77 VWLLSAPPYQ---EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                               SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                               Gaps
                                               19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                              : :|: |||| ||: |||: || :||: |
TLSALYARRRSYLFLGGILMSAMSLML-LSSLGNLFFGSVWLFQANLYMGLVVMCGFVLF
Score 491.5; DB 22; Length 236;
Pred. No. 1e-49;
3; Mismatches 72; Indels 7;
                                                                                                                                                                                               DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKK 245
                                                                                                                                                                                                             Lung cancer associated polypeptide sequence SEQ ID 516.
                     , 72;
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38.6%; Scc
42.9%; Pre
tive 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US05918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270
                                                                                                                                                                                                                                                                                                                                    (first entry)
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587514/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens, useful for
such as lung cancer
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF18054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055180-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                    14-MAR-2001
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                                                                                                                                                                                                                                                                                                             AAB58178;
  Query Match
             Best Local
Matches 9
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gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAF86459 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                          63 I--GGILTTMACMGSMVWILLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 IVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFK 178
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                  17 GIMNIFD-----RKINFDALLKFSHITPSTQQHLKKVYASFALCMFVAAGAYVHWVTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWN
                                                                                                                                                                                                                                                                                                                                                                                                                   71 FIQAGLLSALGSLILMIWLMATPHSHETEQKRLGLLAGFAFLTGVGLGPALEFCIAVNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 FELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                  Length 255
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                Query Match 38.0%; Score 483.5; DB 21; Best Local Similarity 41.1%; Pred. No. 1e-48; Matches 102; Conservative 54; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bax inhibitor; BI-1; human; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW73136 standard; Protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US05015.
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bax inhibitor BI-1
                                                                                                                                                           255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEEKKKKR 246
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                                                                                                                    sednences
                                                                                                                                                           Sequence
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This is the amino acid sequence of an inhibitor protein, termed .

B1-1, of the pro-apoptotic protein Bax. Nucleic acids encoding
B1-1, feee AAVS9067) and B1-2 (see AAVS9068) were identified by
suppression of Bax-induced death of yeast cells transformed to
suppression of Bax-induced death of yeast cells transformed to
express human Bax. A human HepG2 cDNA library was used for library
containing. The invention provides vectors, optionally expression
or viral vectors, containing B1 nucleic acids, and host cells
containing these vectors. The nucleic acids encoding B1-1/B1-2 can
be used to increase expression of these proteins in cells, or
antisense molecules prepared from them used to decrease expression.
In these ways, cellular apoptotic activity may be modulated. The
B1S and peptides portions are useful to detect, e.g. another B1 or a
member of the Bc1-2 family in biological samples. They are
cepecially useful in assays to identify agents (e.g. organic
cepecially useful in assays to identify agents (e.g. organic
college or peptides; claimed) modulating the specific association
of B1-1/B1-2 with a second protein (e.g. a B1, an anti-B1 antibody
or a Bc1-2 family protein (e.g. Bax) (claimed)) e.g. in screening
or attivity. The agents can then be contacted with cells to modulate
cellular apoptotic activity (claimed). Bax overexpression is
activity apoptotic activity (claimed). Bax overexpression is
cellular dord injuty, Parkinson's disease and Alzheimer's disease.
Antibodies raised against the B1s and peptides are also useful e.g.
to detect/quantify B1s in biological samples.
                                                                               Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate cellular apoptotic activity or identify agents altering BI-1 or BI-2 binding which can modulate apoptotic activity
                                                                                                                                                                                   Claim 14; Fig 1; 80pp; English
                    WPI; 1998-531519/45.
N-PSDB; AAV59067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 AA;
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Claim 11; SEQ ID No 4128; 2922pp; English.

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                                                                                                                       77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                    Gaps
                                                                                          68
                                                               9
                                                                               135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF
                                                                                                                                                                                                SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM
                                   7;
      Length 237;
                                                                                                                                                                                                                                        DTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                       74; Indels
      DB 19;
      37.5%; Score 477.5; DB 1
42.2%; Pred. No. 4.8e-48;
ive 53; Mismatches 74
Query Match
Best Local Similarity 42.2<sup>3</sup>
....hes 98; Conservative
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Human, ovarian antigen, ovary, ovarian, breast, cancer, tumour, ovarian cancer, breast cancer, tumour, reproductive system disorder, infertility, pregnancy disorder, anovulation, polycystic ovary syndrohe, PCOS, ovarian cyst, dysmenotrhoea, endocrine disorder; infection; inflammatory condition, immune disorder; blood disorder;
                                                                                                                Human ovarian antigen HPDWT56, SEQ ID NO:4128.
  ABP42996 standard; Protein; 245 AA
                                                                            (first entry)
                                                                              22-AUG-2002
                                      ABP42996;
& MANAGE KAK SKA
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cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2000; 2000US-209467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABQ56073
                                                                                                                                                                                                                                                                                                         WO200200677-A1
                                                                                                                                                                                                                                   Homo sapiens.
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une invention relates to 2.1% novel numban ovarian antiques (AMPF41024-C ABP43228) and to CDMAs encoding them (ABD54111-ABD56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical comprises polypeptides in the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antique polymucleotides, antibodies against human ovarian antiques of ovarian antique polymucleotides and polypeptides in diagnosing, cof ovarian antique polymucleotides and polypeptides in diagnosing, cof ovarian antique polymucleotides and polypeptides in diagnosing, cof ovarian include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, collycystic ovary syndrome, ovarian or breast origin, reproductive system disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic consortities onlycystic ovary syndrome, ovarian orysts, and dysmenorthoea), endocrine disorders, infertility, disorders of pregnancy, anovulation, and toxic consortities, and dysmenorial or disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic consortities, and dysmenorial and collycystic ovary system disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), respiratory disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and unimary system disorders. Ovarian antigen polypeptides and proceeding may be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies constituted as human ovarian antigen of the invention. Sequence representes a human ovarian antigen of the invention construction of individual patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO car fibe sequence care for this patent did not form procession or effective or to prepare a invention relates to 2175 novel human ovarian antigens (ABP41054-

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63 I -- CGLLTTMACMGSMVWLLSAPPYQ -- EQKRVALLMAAALFEGASIGPLIELGINFDPS 118
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                        GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMN 62
                                                                                                                                                                                                                                                             78; Indels 11;
                                                                                                                                                                                                                                         DB 23; Length 245;
                                                                                                                                                                                                                                         26.1%; Score 331.5; DB 2 34.8%; Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                             Local Similarity
nes 72; Conservat
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NI--GGILLTTMACMGSMVWLLSAPPYQ--EQKRV--ALLMAAALFEGASIGPLI---ELG 112
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ABB63069
ID ABB63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
     119 IVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFK 178
                        Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 277;
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                                                                                              190 ANLYXGLVVMCGFAFLILNSLLKRPNM 216
                                                                         179 FELYFGLLVFVGYIVFDTQEIIEKAHL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 262; 765pp; English.
                                                                                                                                                                                                  AAU30218 standard; Protein; 277 AA
                                                                                                                                                                                                                                                                                                         Novel human secreted protein #709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0552929
2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rang YT, Liu C, Drmanac
                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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26-JAN-2001;
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                                                                                                                                                                                                                                  AAU30218;
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Matches
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AAU30218
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13;

88; Indels 34;

93; Conservative

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3 GFTSFPDSQSASRNRWSYDSLKNFRQISPLV-QTHLKQVYLTLCCALVASAAGAYLHITHW.61

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Gaps
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                                                                                                                                                                                                                                                                             190 FWIPFWVFQANLYVGLVVMCGFVLFDTQLIIEKARQGDQDYNLWHCIDLFLDFITVF---
                                                                                                113 INFDPSIVFGAFVGCA-VVFGCFSAAAMLARR-REYLYLGGLLSSGVSLL-FWLHFASSI
                                                                                                                                                                                                                                      170 FGGSMAVFKFELYFGLLVFVGXIVFDTQEIIBKAHLGDMDY-VKHALTLFTDFGAVFVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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34.4%; Pred. No. 2.2e-28;
iive 48; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                               247 ----QKNSMKDPGPXMKKDKKKRRN 268
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Best Local Similarity 34.4 Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
N-PSDB; ABL07172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL16176-ABL36511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                       GKYLYLGGMLVSVINTMALLSLFNMVF-KSYFVQVTQLYVGVFWMAAFIVYDTQNIVEKC 1999
                                          -----KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARR 143
                                                                                     144 REYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEITEKA 203
              PLVQTHLKQVYLTLCCALVASAAGAYLHI -- LWNIGGLLTTMACMGSMVWLLSAPPYQEQ 88
                                                                                                                                                                                                                                                                                                 Drosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Score 192; DB 22; Length 305; larity 25.7%; Pred. No. 5.2e-14; Conservative 49; Mismatches 87; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 747; 21pp + Sequence Listing; English.
                                                                                                                                204 HLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKBEKKKKRR 247
                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                            ABB57985 standard; Protein; 305 AA.
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
interactions -
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N-PSDB; ABL02088.
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(ABB57737-ABB72072)
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85 HATYAYFGASCGVTAASAVAFFQSDAMMALMTRSGWVASLVTLGLVMLSGSIAQGLEYQP 144
                                                                                                                                      145 GFGAKQLAWLVHCAVL-GAVLAPMCLLG----GPILTKALLYTSGIVGALSTVAACAPSE 199
                                                                                                                                                                                                                                              145 EYLYLGGLLSSGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQ 197
                                                                                          85 YOEOKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRR 144
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                                                                                                                                                                                                                                                                                                                                                            198 EIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILLIMLKNASEKEEKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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Best Local Similarity 26.5%; Pred. No. 1.4e-11;
Matches 56; Conservative 46; Mismatches 77; Indels 32
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11-JUL-2000; 2000US-0614150.
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N-PSDB; ABL02901.
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40; "Gaps"

36 HLKQVYLTLCCALVASAAGAY----LHILWNIGGLLTTMACM-----GSMVWLLSAPP 84

Best Local Similarity Matches 61; Conserv

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growth hormone (GH) in brown adipose tissue, by assaying the levels of specific gene transcripts. The genes of interest are those encoding glucosephosphate isomeraes. The genes of interest are those encoding glucosephosphate isomeraes, The genes of interest which are an encoding chair trans-Golgin etwork protein, alpha-enolase, proteasome theta adiporte lipid binding protein, medium chain acyl-CoA debydrogenase, anitochondrial NADH-ubiquinone oxidoreductase, mitochondrial cytochrome B or any of the genes Ng-GlisK2, Ng-119K65, Ng-119K65, Ng-119K65, Ng-119K65, Ng-119K65, This is useful for diagnosing abnowmal levels of GH or predicting changes in brown adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention provides a method of diagnosing abnormal levels of
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                                                          192 VHCAIL-GAVIAPICFMG---GPILTRAALYTGGIV-GGLSTIAACAPSDKFLYMGGPLA 246
                                                                                                            155 SGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHL-- 205
                                                                                                                                  247 IGLGVVFASSLASMUPPTTALGAG---LASMSLYGGLVLFSGFLLYDTQRMVRRAEVYP 303
132 CVLTAAAAAATFRSHRLLELASRGGILATIASLALVIGSGAVARSIEYQPGLGAKHLAWA 191
                                    95 MAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse brown adipose tissue clone 42 protein.
                                                                                                                                                                                    206 ----GDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                 304 QYSYTPYDPINASMSIYMDVLNIFIRIVTIL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth hormone; brown adipose tissue.
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                                                                                                                                                                                                                                                                                                                     AAB49311 standard; Protein; 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-2000; 2000WO-US12145
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21; Length 346; 11; 84; Indels 32; g

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42 LILCCALVASAAGAYLHIL----W-NIGGLLTTWACMGSMVWLLSAPPYQEQKRVALLMA 96

Query Match
Best Local Similarity 25.9%; Pred. No. 1.9e-11;
Matches 57; Conservative 47; Mismatches 84;

97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSG 156

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Db 198 SGVM-GAVVAPLILIG---GPLILRAAWYTAGIV-GGLSTVAMCAPSEKFLNMGAPLGVG 252

Qy 157 VSLLFWLHPASSIFGGSM------AVFKPELYFGLLVFVGYIVPDTQEIIEKAHLG 206

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Qy 207 DM-----DYVKHALILFTDFGAVFVRILIIMLKNASEKE 240

Db 307 PMYGAQKYDPINSMLTINFTNINFMRVATMLATGSNRKK 346

Search completed: May 25, 2003, 12:20:50

Job time: 64 secs
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Appl
Sequence 83, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 493, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 28, Appli
Sequence 30, Appli
Sequence 31, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 17, Appli
                                                                                 May 25, 2003, 12:19:44 ; Search time 35 Seconds (without alignments) 208.482 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7,
Sequence 9,
Sequence 2,
Sequence 10,
Sequence 10,
Sequence 10,
                                                                                                                                         US-09-955-526-4
1272
1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*

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. /cgn2 = /ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                           262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext
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seq length: 200000000
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Match Length
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Perfect score:
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No.
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Sequence 2, Appli Sequence 11, Appl Sequence 11, Appl Sequence 5241, Appl Sequence 22, Appl Sequence 23, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl		programmed cell the modification of forestry plant devel	Length 213; Indels 3; Gap	P.	ртовітаканцармруукнадт 216 	programmed cell the modification of forestry plant devel
4 US-09-387-699-2 4 US-07-9-641-259B-2 1 US-07-9-9-1258B-2 1 US-07-9-134-001C-5241 4 US-09-372-4228-32 4 US-09-372-469-22 4 US-09-568-460-22 5 4 US-09-568-480-22 5 4 US-09-568-480-22 5 4 US-09-568-480-22 5 4 US-09-568-480-22 6 4 US-09-568-480-22 7 US-09-568-480-22 6 4 US-09-568-480-22 7 US-09-568-480-22 7 US-09-134-001C-5530 1 US-09-134-001C-5530 1 US-08-08-134-11 1 US-09-134-001C-530 2 US-08-08-134-11 1 US-09-134-001C-530 2 US-08-08-134-11 1 US-08-134-001C-530 2 US-08-08-134-11	ALIGNMENTS cation US/09325932A	affecting heir use in %325,932A brsion 3.0	core 688.5; red. No. 4. Mismatche	OVYLTLCCALVASAAGAYLHILMNIGGLLTTMACMGSMVWLLSAPPYGEOKRVALLMA	VGYIVF : LGYIIF 247 212	32A affecting eir use in
28 79 6.2 335 29 79 6.2 335 315 29 79 6.2 335 315 20 20 315 315 20 20 315 315 315 315 315 315 315 315 315 315	RESULT 1 US-09-328-87 Sequence 87, Application 1 Patent No. 6451604 GENERAL INFORMATION:	APPLICANT: Flinn, Barry APPLICANT: Labam, Annette TTILE OF INVENTION: Compositions TITLE OF INVENTION: death and th FILE REFERENCE: 1022 CURRENT APPLICATION NUMBER: US/05 CURRENT APPLICATION NUMBER: US/05 CURRENT APPLICATION NUMBER: US/05 NUMBER OF SEQ ID NOS: 206 SOFTWARE: FREESEQ for Windows V6; SEQ ID NO 87 LENGTH: 213 TYPE: PRT ORGANISM: Pinus radiata	US-09-325-932A-87 Query Match Best Local Similarity 64 Matches 137; Conservativ	Oy 39 QVYLTLCCALVASAAGAYLHILMNI	OY 157 VSLLFWLHFASSIFGGSMAVFKELYFGLLVF	RESULT 2 US-09-325-932A-88 US-09-325-932A-88 Sequence 88, Application US/093259; Patent No. 6451664 GENERAL INFORMATION: APPLICANT: Flinn, Barry APPLICANT: Lasham, Annette TITLE OF INVENTION: Compositions; TITLE OF INVENTION: death and th

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STREET: 43/C
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Best Local Similarity 42.2%; Pred. No. 3.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7/19, Gaps. 14;
                                                                                                                                                                                                                                                                                                                                                                                     61 WNIGGLITTWACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                          Query Match
39.3%; Score 499.5; DB 4; Length 140;
Best Local Similarity 66.2%; Pred. No. 4.7e-51;
Matches 100; Consérvative 14; Mismatches 26; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                           1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
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US-08-818-514-3
US-08-818-514-3
Sequence 3, Application US/08818514
Factor No. 5837838
FAPLICANT: Reed, John C.
APPLICANT: X. Qunli
ITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FGAFVGCAVVFGCFSAAAMLARREYLYLGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ISAFVGSALAFACFSGAA------CWLGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REPERENCE/DOCKET NUMBER: P-LJ 2446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States
                                                                                                                                                    ; ORGANISM: Pinus radiata
US-09-325-932A-88
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                                                                                                             TYPE: PRT
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                                                                                            SEQ ID NO 88
LENGTH: 140
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77 VWLLSAPPYO--EOKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
9 NFDALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVHMVTHFIQAGLLSALGSLILM 68
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                                                                                                                                                                                                                                                                                                                                                                  195 DIQELIEKAHLGDMDYVKHALTLFIDFGAVFVRILLIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                                                                          188 DIQLIIEKAEHGDODYIWHCIDLFLDPITVFRKLMMILAMN--EKDKKKEKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, John C.
APPLICANT: Ru, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION TO THE CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carlbyn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-LJ 3209
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-115-934A-3

Sequence 3, Application US/09115934A

Patent No. 6130317

GENERAL INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
: United States
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BARLIER
                                                                                                                                                                                                                            APPLICANT: Cooke, Michael Paul
APPLICANT: Cooke, Michael Paul
APPLICANT: Cooke, Michael Paul
APPLICANT: Holness, Claire
APPLICANT: Sirenko, Oksana
TITLE OF INVENTYON: No. 6451558èl Genes in the Control of Hematopoiesis
FILE REFERENCE: 4-30629454XS
CURRENT APPLICATION NUMBER: US/09/362,123A
CURRENT APPLICATION NUMBER: 09/128,310
PRIOR APPLICATION NUMBER: 09/128,310
PRIOR FILING DATE: 1998-098-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 345
TANDER: 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 KFLNMGAPLGVGLGLV---FVSSL--GSMFLPPTTVAGATLYSVAMYGGLVLFSMFLLY 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 HSTYMYLAGSIGLTALSALAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 Q---KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAMLARRR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 EYLYLGGLLSSGVSLLFWLHFASSIFGGSM------AVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 HLKQVYLTLCCALVASAAGAYLH--ILWNI---GGLLT---TWACMGSMVWLLSAPPYQE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQEIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILLIMLKNASEKE 240
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                                 13.0%; Score 165; DB 4; Length 345; ilarity 26.3%; Pred. No. 4.1e-11; Conservative 47; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE SPERENCES:
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
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Patent No. 6420526
                                                                                                                                                           US-09-362-123A-2
; Sequence 2, Application US/09362123A
; Patent No. 6451558
; RENERAL INFORMATION;
; APPLICANT: Cooke, Michael Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 61; Conserv
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FILING DATE: 1997-05-23
APPLICATION WOMBER: 60/047,492
APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: 60/043,568
LING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATE: 1997-04-11
ION NUMBER: 60/043,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/043,671
                                                                                                                                                                                                                                                                                            047,618
                                                                                                                                                                                                                                                                                                                                                                             60/047,592
                                                                                                                                                                                                                                                                                                                                                                                                 LING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICATION NUMBER: 60/047,596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/047,587
LON NUMBER: 60/0
                                                                                                                                                                                                           APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LING DATE: 1997-05-23
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                                                                                                                                                                                            LING DATE: 1997-05-
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BARLIER PELICATION WHORER: 60/056,89
ERALLIER FILING DATE: 1197706-22
ERALLIER PELICATION WHORES: 60/056,89
ERALLIER PELICATION WHORES: 60/056,89
ERALLIER FILING DATE: 1197706-22
ERALLIER RAPLICATION WHORER: 60/056,894
ERALLIER RAPLICATION WHORER: 60/056,994
ERALLIER PALLICATION WHORER: 60/056,994
ERALLIER FILLING DATE: 1997-06-22
ERALLIER FILLING DATE: 1997-06-23
ERALLIER FILLING DATE: 1997-06-23
ERALLIER FI
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145 EYLYLGGLLSSGVSLLFWLHFASSIFGGSM------AVFKFELYFGLLVFVGYIVF 194 Query Match
13.0%; Score 165; DB 4; Length 346;
Best Local Similarity 26.3%; Pred. No. 4.1e-11;
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 88 O---KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRR 144 36 HLKOVYLTLCCALVASAAGAYLH--ILWNI---GGLLT---TMACMGSMVWLLSAPPYOE 87 DIQEIIEKAHLGDM------DYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240 Sequence 89, Application US/09247155A
Patent No. 631292
GENERAL INFORMATION:
APPLICANT: Duclert, Aymeric
APPLICANT: Boughaleret, Lydie
APPLICANT: Boughaleret, Lydie
TITE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273 RESULT 7 US-09-247-155-89 195 294 ઠે a ઠ g ò

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APPLICATION. ...

APPLICATION. ...

ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 96,749

REJECOMMUNICATION INFORMATION:
TELEPHONE: (415) 845-0555

TELEPHONE: (415) 845-0556

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids

"WDE: amino acids
"WDE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 ALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 ALQIYTDIIVIFTFVLQLM 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
INMEDIATE SOURCE:
  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
                                                                                                 US-08-794-216-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AALFEGASIGPLIELGIN----------FDPSIVFGAFVGCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 VVFGCFSAAA-MLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELY---- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 TVF--FGLTVYTLQSKXDFSKFG----AGLFALLWILCLSGF------LKFFLYSEIME 179
                                                                                                                                                                                                                                                                   Query Match (8.8%; Score 112.5; DB 4; Length 238;
Best Local Similarity 23.3%; Pred. No. 3.7e-05;
Matches 54; Conservative 36; Mismatches 67; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                  50 ASAAGAYLHI-----LWNIGGLLTTMACMGSMVWLLSAPPYQEQKRV-----ALLMA 96
                                                                                                                                                                                                                                                                                                                                                                                                              21 SSVASATVHIRMAFLRKVYSILSLQVLLTTVTSTVFL----YFESVRTFVHESPALIL- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 IVLAAAGALLFCGFIIYDTHSLMHK--LSPEEYVLAAISLYLDIINLFLHLL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 314 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,216
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 14
FILING DATE: Herewith
CLASSIFICATION NUMBER: 54
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Ludy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION NUMBER: 415,855,4456
TELEFAX: 415,845,4166
TELEFAX: 415,845,4166
TELEFAX: 415,845,4166
TELEFAX: 416,845,4166
TELEFAX: 416,845,4166
TELEFAX: 416,845,4166
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
NUMBER OF SEQ ID NOS: 182
SCPTWARE: Patent.pm
SEQ ID NO 89
LENGTH: 238
TYPE: PRT
ORGANISM: HOMO Sapiens
FEATURE:
                                                                                                                                                                    ) NAME/KEY: SIGNAL
; LOCATION: -53..-1
US-09-247-155-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-794-216-1
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41 YLTLCCALVASAAGAYLHILWNIGGLLTTMACMGSWWLLSAPPYQEQKRVALLMAAALF 100
                                                                                                                                                                             148 YLILAC-----CQGPRRRFPWNIILLTTFRAMGFWTGTISS-MYQTK---AVIIAMIIT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                   244 QYVYWLKM------LYAALGAICFTLFLAYDTQLVLGNRKHTISPEDYITG 288
                                                                                                                                                                                                                                                            101 EGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAMLARRREYLYLGGLLSSGV--- 157
                                                                                                                                                                                                                                                                                                                           199 AVVSISVTI---FCFQTKVDFTSCTGLFCVLGI-------VLLVTGIVTSIVLYF 243
                                                                                                                                                                                                                                                                                                                                                                                             158 SLLFWLHFASSIFGGSMAVFKFELY--FGLLVFVGYIVFDTQEII--EKAHLGDMDYVKH 213
Query Match 8.6%; Score 109; DB 2; Length 311; Best Local Similarity 24.6%; Pred. No. 0.00014; Matches 49; Conservative 28; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESULY
Sequence 1, Application US/08749289
Sequence 1, Application US/08749289
Fatent No. 5955301
FATENT No. 5955301
FAPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, NOWEL HUMAN GLUTAMATE-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
ADDRESSE: INCYTE Pharmaceuticals, Inc.
STREET: 314 Porter Drive
CITY: Palo Alco
STATE: California
CONDTRY: USA
ZIP: Palo Alco
STATE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRESSES
SOFTWARE: FRESSES
CURRENT APPLICATION NUMBER: US/08/749,289
FILING DATE: Filed Herewith
CLASSFICATION NUMBER:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
ATLING APPLICATION NUMBER:
ATLING APPLICATION NUMBER:
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TYPE: PRT
CRGANISM: Zea mays
US-09-372-422A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-794-216-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 LVRGHITKLRALLYVAAQLLASSLACIL-LRYLSGGWVTPVHALGAGI-----RPMQGLV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 APPYQEQKRVALLMAAALFEGASIGPLI-ELGINFDPSIVFGAFVGCAVVFGCFSAAAML 140
                                                                                                                                                                                                                                                                                                                          244 ASFYNTE---AVIMAVGITTAVCFTVVIFSMQTRYDFTSCMGVLLVSMVVLFIFAILCIF 300
                                                                                                                                                                                                                                                                                                                                                                                        141 ARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEII 200
                                                                                                                                                                                                                                                                                                                                                                                                                  185 AEVKĞFVRENVWTYYVSYAVFFISLIVLSCCGDFRRKHPWNLVALSVLTASLSYMVGMI- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 LVQTHLKQV --YLTLCCALVASAAGAYLHILWNIGGLLFTWACMGSMVWLLSAPPYQEQK 89
                                                      Gaps
                                                                                                                                                                                            50 ASAAG-----AY----LHIL------WNIGGLLTTWACMGSMVWLLS 81
                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
7.6%; Score 96.5; DB 4; Length 257;
Best Local Similarity 24.1%; Pred. No. 0.0031;
Matches 40; Conservative 33; Mismatches 58; Indels 35
Ouery Match
8.4%; Score 107; DB 2; Length 369;
Best Local Similarity 20.8%; Pred. No. 0.0003;
Matches 57; Conservative 41; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 SMNPARS----FGPAMATGVWTNHWVYWIGPLLGGSLAGFVYESLF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Rudolf Jung
APPLICANT: Rudolf Jung
APPLICANT: Rudolf Jung
APPLICANT: Prancols Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION UNMER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: RatiseQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/09372422A
Patent No. 6131370s.
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                  2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 -- EKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
108-09-372-422A-28
'Sequence 28, Application US/09372422A
'Patent No. 6313375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-372-422A-30
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Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 56; Conservative 48; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 --LVOKMHEAAAQWGSLTTISPCVVAHASCLF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09372422A Patent No. 6313375 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             319 VFAALNLYTDIINIFLYILTII 340
                                                                                                                                                                                                                                                                                                                                                                                   211 VKHALTLFIDFGAVFVRILLIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-26
                                                                                                                                       61 WNIGGL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-372-422A-26
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                                                                                                                                                                                                                                                           161 GEVKGFVRANVWTYYVSYAIFFISLIVLSCCGDF------RKKHPWNLVALSILT- 209
                                                                                                                                                                                                                                                                                                      103 ASIGPLIELGINF--DPSIVFGAFVGCAVVFGCFSAAAM-LARRREYLYLGGLLSSGVSL 159
                                                                                                                                                                                                                                                                                                                                  210 ISLSYMVGMIASFYNTEAVIMAVGITTAV---CFTVVIFSMQTRYDFTSCMGVLLVSVVV 266
                                                                                                                                                                                                                                                                                                                                                                                   160 LFWLHFASSIFGGSMAVF----KFELYF---GLLVFVGYIVFDTQEII--EKAHLGDMDY 210
                                                                                                                                                                                                                        61 WNIGGL------LTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEG 102
                                                                                                  Gaps
                                                                                                                                       2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL-VASAAGAYLHIL 60
                                                                                                  63;
                                                              Length 516;
                                                         ; Score 94.5; DB 2; Length 51; Pred. No. 0.014; 48; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-749-289-3

Sequence 3, Application US/08749289

Fatent No. 1895301

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Coleman, Roger

TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM POS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,289
FILING DATE: Filed Herewith
CLASSIFICATION: DATA:
PRIOR APPLICATION: DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INPORMATION:
NAME: B.11ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET UNMBER: PF-0:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 855-0555
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 VKHALTLFTDFGAVFVRILLIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 VFAALNLYTDIINIFLYILTII 340
                                                         Query Match
Best Local Similarity 21.4%;
Matches 56; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: USA
  ; CLONE: 238267
US-08-794-216-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-749-289-3
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DB 2; Length 516;

7.4%; Score 94.5;

Query Match

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9
14;
                                                                                                                                                                                                                                                                               103 ASIGPLIELGINF--DPSIVFGAFVGCAVVFGCFSAAAM-LARRREYLYLGGLLSSGVSL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 KRVALLMAAALF-----EGASIGPLIELGINFDPSIVFGAFVGC-AVVFGCFSA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 VMEVILTESLLEVIYAMILDPRSQVRAIGPLLT------GLIVGANSLAGGNFTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 AAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDT 196
                                                                                                                                              -----ITTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEG 102
  63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 LVQTHLKQVYLTLCCA---LVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSAPPYQEQ 88
                                                  2 EGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCAL-VASAAGAYLHIL 60
                                                                                                                                                                              160 LFWLHPASSIFGGSMAVF --- KFELYF --- GLLVFVGYIVFDTQEII -- EKAHLGDMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 94; DB 4; Length 272; llarity 22.6%; Pred. No. 0.0067; Conservative 32; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rudolf Unng
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
TITLE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ 1D NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
TYPP: ...
  95; Indels
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US-07-879-617A-12
Sequence 12, Application US/07879617A
; Patent No. 5580775
; GENERAL INFORMATION:
; APPLICANT: Fremeau Jr., Robert T.
; APPLICANT: Caron, Marc G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 VASAAGAYLHILWNIGGLLTTWACWGSWVWLLSAPPYQEQKRVALLMAAALFEGASIGPL 108
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APPLICANT: Blakely, Randy D.

TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES:

ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 3009
CONTRY: U.S.
ZIP: 3009
CONTRY: U.S.
ZIP: 3009
CONTRY: U.S.
ZIP: 3009
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                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,617A
FILING DATE: 19920501
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADST, PALTER L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELEFAX: 404-815-6598
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
'ENGTH: 607 amino acids
'ENGTH: 607 amino acids
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NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note= "Leucine zipper motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: Active-site
; LOCATION: 116..117
; OTHER INFORMATION: /note= "Leucine zipper motif"
US-07-879-617A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Active-site
LOCATION: 95..96
OTHER INFORMATION: /note= "Leucine zipper motif"
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OTHER INFORMATION: /note= "Leucine zipper motif"
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TISSUE TYPE: Brain - serotonin transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 607 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPOLLOGY: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity 22.7%
Matches 55; Conservative
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NAME/KEY: Active-site
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Oy 165 FASSIFGGSMAVFKELYFG-LLVFVGYIVFDT---QEIIEKAHLGDMDYVKHALTLFTD 220

b) 306 AAAQIF-----FSLGPGFGVLLAFASYNKFNNNCYQDALVTSVNCMTSFVSGFVIFTV 359

Cy 221 FG 222

Db 360 LG 361

Search completed: May 25, 2003, 12:24:35

JOb time: 37 secs
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FGAFVGCAVVFGCFSAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
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Best Local S:
Matches 248
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Sequence 274, App
Sequence 18, Appl
Sequence 32, Appl
Sequence 6, Appli
Sequence 2, Appli
Sequence 273, Appli
Sequence 87, Appli
Sequence 88, Appli
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Sequence 88, Appli
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                                                                                                                                                     May 25, 2003, 12:22:59 ; Search time 54 Seconds (without alignments) 455.460 Million cell updates/sec
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Sequence 20,
Sequence 2, A
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1272
1 MEGFISFPDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248
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1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW FUB.pep:*
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14: //cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-167-015-16
US-10-167-015-18
US-10-167-015-18
US-10-167-015-32
US-10-167-015-34
US-10-167-015-4
US-10-167-015-4
US-10-187-015-4
US-10-187-015-4
US-10-219-220-87
US-10-219-220-88
US-10-219-220-88
US-10-219-220-88
US-10-219-220-88
US-09-99-239-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                                                                                          OM protein
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                                                                                                                                                             Run on:
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61 WNIGGLLTIMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEGFTSFFDSQSASRNRWSYDSLKNPRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                               Sequence 2, Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/0995526;
Publication No. US20030009785A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Plant Cytoprotective Genes and Methods
TITLE OF INVENTION: Plant Cytoprotective Genes and Methods;
TITLE OF INVENTION: Of Using Same;
FILE REFERENCE: P-LJ 480 Same;
CURRENT APPLICATION NUMBER: US/09/955,526
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ilarity 100.0%; Pred. No. 5.4e-115;
Conservative 0; Mismatches 0;
                 US-09-990-4456-2
US-09-991-1811-2
US-09-991-1811-2
US-09-993-653-2
US-09-990-438-2
US-09-990-586-2
US-09-990-566-2
US-09-990-7428-2
US-09-990-7428-2
US-09-990-7111-2
US-09-990-7111-2
US-09-991-172-2
US-09-991-172-2
US-09-991-172-2
US-09-991-172-2
US-09-990-743-2
US-09-990-7443-2
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: LENGTH: 248

: TYPE: PRT

: ORGANISM: Lycopersicon esculentum

US-09-955-526-4
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181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 GLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKK 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ISAFVGSALAFACFSGAAMLARREYUXLGGLLSSGLSMLWMLHFASAVFGGSAAIFKFE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GGLLTTMACMGSMVWLLSAPPYQEQXRVALLMAAALFEGASIGPLIBLGINFDPSIVFGA 123
                                                                                                                                                                                                                                                                                                                              61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                 1 MDAFASLFQS---SGKGWSHDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGGAYLHLM 57
                                                                                                                                                                                                         1 MEGPISFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
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US-10-167-015-18

Sequence 18, Application US/10167015

Sequence 18, Application US/10167015

Publication No. US20030056249A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Acceded, Pedro A. Navarro

APPLICANT: Tac. Yunin Tac. Yunin Thereof

FILE REFERENCE: 138

CURRENT APPLICATION NUMBER: US/10/167,015

CURRENT PILING DATE: 2001-06-12

MUMBER OF SEQ ID NOS: 34

SEQ ID NO 18

LENGHRAE: FastSEQ for Windows Version 3.0

LENGHRAE: Acceded A. Navarro

LENGHRAE: Acceded A. Navarro

BENGHRAE: Acceded A. Navarro

                                                                                    Query Match 75.7%; Score 963.5; DB 9; Length 247; Best Local Similarity 74.4%; Pred. No. 3.1e-85; Matches 186; Conservative 27; Mismatches 32; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.1%; Score 955; DB 9; Length 261; Best Local Similarity 73.3%; Pred. No. 2.2e-84; Matches 178; Conservative 36; Mismatches 27; Indels
; ORGANISM: Eucalyptus grandis
US-10-219-220-274
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CORGANISM: Glycine max
US-10-167-015-18
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                                                                                                                 RESULT 2
US-10-167-015-16

Sequence 16, Application US/10167015
Publication No. US20030056249A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Tac. Yumin Tac.
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use;
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use;
TITLE REFERENCE: 138
CURRENT FILING DATE: 2002-06-11
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFWWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LEMONTH: 244
TYPE: PRT
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241 EKKKKRRN 248
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240 KKRRD 244
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GAYLHILWNIGGLLTTWACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                  54 GAYLHILWNIGGLLTTWACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEGFTSFFDSQSASR-----NRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAA 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10167015;
Publication No. US20030056249A1
GENERAL INPORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Acevedo, Pedro A. Navarro
APPLICANT: Tao, Yumin
APPLICANT: Tao, Yumin
TILE OF INVENTION: Thereof
FILE REFERENCE: 1388
CURRENT APPLICATION THEREOF
FILE REFERENCE: 1388
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
FRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.1%; Score 878.5; DB 9; Length 285; 65.8%; Pred. No. 5.8e-77; ive 37; Mismatches 42; Indels 9;
                                                                                                                                            69.1%; Score 878.5; DB 9; Length 258; 65.8%; Pred. No. 5:2e-77; Live 37; Mismatches 42; Indels 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 LKNASEK-EEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LKNAADKSEDKRRKRRS 257
                                                                                                                                                   Query Match
Best Local Similarity 65.84
Matches 169; Conservative
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9; Conservative
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CRGANISM: Zea mays
US-10-167-015-6
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Matches 169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 VFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AFFSASSASAPYGYGAGGWSYDSLKOYFRQITPAVQTHLKLVYLTLCAALASSAVGAYLHV 62
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; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamn, William J.
APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
                                                                                                                                          USEQUENCE 32, Application US/10167015

PUDIcation No. US20030056249A1

SEQUENCE 32, Application US/10167015

PUDIcation No. US20030056249A1

SEQUENCE INFORMATION:

APPLICANT: Simmons. Carl R.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Aceved. Pedro A. Navarro

APPLICANT: Aceved. Pedro A. Navarro

APPLICANT: Aceved. Pedro A. Navarro

APPLICANT: Aceved. Tao, Yumin

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

CURRENT APPLICATION NUMBER: US 60/297,478

FRICH FILING DATE: 2001-06-12

PRIOR FILING DATE: 2001-06-12

PRIOR FILING DATE: 2001-06-12

SEQ ID NO 32

IENGTH: 252

TYPE: PRT

ORGANISM: Zea mays

US-10-167-015-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.5%; Score 884.5; DB 9; Best Local Similarity 66.4%; Pred. No. 1.3e-77; Matches 166; Conservative 36; Mismatches 41.
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                                           243 KKR 245
         244 KKR 246
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US-10-167-015-34
                                                                                                          RESULT 5
US-10-167-015-32
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CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/297,478
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.2'
Matches 153; Conservative
                                                                                                                                                                                                                Best Local Similarity 64.8
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-273
                                                                                                                         ; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 KKRR 247
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US-10-219-220-273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 VFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKF 179
                       173 SMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.1%; Score 853; DB 9; Length 252; Best Local Similarity 65.1%; Pred. No. 1.4e-74; Matches 162; Conservative 32; Mismatches 43; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10167015
Publication No. US2030056249A1
GENERAL INFORMATION
APPLICANT: Simmons, Carl R.
APPLICANT: Johal, Gurmukh
APPLICANT: Tao, Yumin
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF UNCATION: Thereof
TITLE OF UNCATION: Thereof
TITLE OF UNCATION: Thereof
                                                                                                                                                                                   Sequence 4, Application US/10167015

Bequence 4, Application US/10167015

Bublication No. US20030056249A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Accevedo, Pedro A. Navarro

APPLICANT: Tao, Yumin

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

CURRENT FILING DATE: 2002-06-11

PRIOR FILING DATE: 2002-06-12

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO.

SEQ ID NO.
                                                                                            ||||::||::|||:
241 LKNAADKSEDKRRKRRS 257
                                                                         233 LKNASEK-EEKKKKRRN 248
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243 VGGQEEEEE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-4
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US-10-167-015-4
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Sequence 273, Application US/10219220
| Publication No. US20030082724A1
| Publication No. US20030082724A1
| GREERAL INFORMATION:
| APPLICANT: Flinn, Barry
| APPLICANT: Lasham, Annette
| TITLE OF INVENTION: Compositions affecting programmed cell
| TITLE OF INVENTION: Compositio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 LVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEK--EEKK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 LHILWNIGGLLTTWACMGSMVWLLSAP--PYQEQKRVALLMAAALFEGASIGPLIELGIN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 FDPSIVEGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSM 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                           7 QSQRRRRAGGSGFESLKRLGHISPAVQSHLKHVYLTLCSALAFSALGAYLHILLNVGGAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEGFTSF----FDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAY
                                                                                                                                                                                                                         11 OSASRNR---WSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKPELYFGL
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61.8%; Score 786.5; DB 9; Length 250; 64.8%; Pred. No. 3.7e-68; tive 34; Mismatches 45; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Indels
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60.2%; Pred. No. 8.6e-67;
tive 39; Mismatches 55;
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61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                  1 MEGFISFEDSQSASRNRWSYDSLKNFRQISFLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                1 MDAFASLFQS---SGKGWSHDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGGAYLHLM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10167015; Publication Wo. US20330066249A1
| Publication Wo. US20330066249A1
| GENERAL INFORMATION:
| APPLICANT: Simmons, Carl R. |
| APPLICANT: Gordon-Xemm, William J. |
| APPLICANT: Gordon-Xemm, William J. |
| APPLICANT: ApplicaNT: Acevedo, Pedro A. Navarro |
| APPLICANT: Acevedo, Pedro A. Navarro |
| APPLICANT: Acevedo, Pedro A. Navarro |
| TITE OF INVENTION: Thereof |
| TITE OF INVENTION: Thereof |
| FILE REFERENCE: 1388 |
| CURRENT APPLICATION NUMBER: US 60/297,478 |
| PRIOR APPLICATION NUMBER: US 60/297,478 |
| NUMBER OF SEQ ID NOS: 34 |
| SEQ ID NO 8 |
| SED IN NO 8 
                                                          39.3%; Score 499.5; DB 9; Length 140; 66.2%; Pred. No. 9.1e-41; tive 14; Mismatches 26; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 141;
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Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Froteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FGAFVGCAVVFGCFSAAAMLARREYLYLGG 151
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| MLKNGADKSEDKKRKKRS 141
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                                                                                               Best Local Simitarity v...
Matches 100; Conservative
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                                                              Query Match
Best Local Similarity
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CORGANISM: zea mays
US-10-167-015-8
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US-09-925-302-516
US-10-219-220-88
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Sequence 88. Application US/10219220
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Genth and their use in the modification of plant development
TITLE OF INVENTION GENTH AND ADDITIONATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
FRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO Set Set Set Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 87, Application US/10219220
Publication No. US20030082724A1
GENERAL INFORMATION:
APPLICAMY: Film, Barry
APPLICAMY: Lashaff, Amette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Cadeth and their use in the modification of plant development
FILE REPRENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
FRIOR FPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 87
LENGTH: 213
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                                                                         97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRRYLYLGGLLSSG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 VSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 AVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.1%; Score 688.5; DB 9; Length 213; 64.6%; Pred. No. 8.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 137; Conservative
                                                                                                                                                                    235 NA-SEKEEKKKKRR 247
                                                                                                                                                                                                                                   241 NADSKSREGKKKRR 254
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ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-87
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US-10-219-220-88
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US-10-219-220-87
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179 FELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIIMLKNASE 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 I--GGLLTTWACMGSMVWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPS 118
                                                                                                                                                                                                                                                                                                                                                                                               17 GTWNIFD-----RKINFDALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVHWVTH 70
                                                                                                                                                                                                                                                                                                                                                         3 GFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMW 62
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Sequence 20, Application US/10167015

Publication No. US20030056249A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Johal, Gurmukh

APPLICANT: Tao, Yumin

TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use

TITLE OF INVENTION: Thereof

FILE REFERENCE: 1388

CURRENT APPLICATION NUMBER: US/10/167,015

CURRENT FILING DATE: 2002-06-11

FRIOR APPLICATION NUMBER: US/0105

WINNERS OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 20

LENGTH: 78

LENGTH: 78

LENGTH: 78
                                                                                                                                                                                                                                                  Query Match 38.0%; Score 483.5; DB 10; Length 255; Best Local Similarity 41.1%; Pred. No. 6.5e-39; Matches 102; Conservative 54; Mismatches 79; Indels 13;
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 516
LENGTH: 255
TYPE: PRT
TYPE: PRT
COGGANISM: Home sapiens
US-09-925-302-516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CAGANISM: glycine max
US-10-167-015-20
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248 KDKKKEKK 255
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US-10-167-015-20
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Search completed: May 25, 2003, 12:31:16 Job time : 55 secs

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171 GGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILI 230

ð g ð

1 | GGSIALFKFELYFGLLVFVGYVIVDTQEIIERAHFGDLDYVKHALTLFTDLAAIFVRILI 60

231 IMLKNASEKEEKKKRRN 248

GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 25, 2003, 12:16:44; Search time 43 Seconds (without alignments) 554.450 Million cell updates/sec Run on:

US-09-955-526-4 1272 1 MEGFISFFDSQSASRNRWSY......LIMLKNASEKEEKKKKRRN 248 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Bax inhibitor-1 [1	TEGT protein - rat			TEGT (testis enhan	probable membrane		probable carrier/t	probable glutamate	probable receptor-	hypothetical prote	mem	integral membrane	conserved hypothet			Ÿ	conserved hypothet	egr	ybhl protein - Esc		netical	ij.	probable glutamate	hypothetical prote	probable glutamte	- 2	conserved hypothet	
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probable membrane	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	ABC transporter (p	N-methyl-D-asparta	ABC transporter (p	hypothetical prote	hypothetical prote	transport permease	transport permease	hypothetical prote	hypothetical prote	conserved membrane	oligodendrocyte tr
AH0954	F71879	B97681	AI2905	H71724	AB1293	853708	AH1664	AG1350	E97723	H86611	A72013	AB1721	T01080	D97248	JC7692
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232	230	260	260	236	629	203	670	225	236	238	238	225	248	231	511
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112 8.8	109.5 8	109 8		108.5	106	104	103.5			101.5				66	98.5

ALIGNMENTS

the Bax Inhibitor-1 (BI-1) gene car Bax inhibitor-1 [imported] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (C,Species: Arabidopsis thaliana (mouse-ear cress) C,Species: Arabidopsis thaliana (mouse-ear cress) C,Species: A-cot-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000 C,Accession: T52449 R;Kawai, M.; Pan, L.; Reed, J.C.; Uchimiya, H. REBS Lett. 464, 143-147, 1999 A,Title: Evolutionally conserved plant homologue of the Bax Inhibitor-1 (BI-1) g A,Reference number: 226078 A,Accession: T52449 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Wolecule type: mRNA A,Residues: 1-247 <KAW> A,Residues: 1-247 <KAW> A,Resperimental source: Columbia C,Genetics: 1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60 Cuery Match 80.5%; Score 1023.5; DB 2; Length 247; Best Local Similarity 77.4%; Pred. No. 1.4e-85; Matches 192; Conservative 31; Mismatches 24; Indels 1; A, Description: suppresses cell death induced by Bax C, Superfamily: human testicular protein TEGT A;Gene: AtBI-1 C;Function: 152449 ò

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61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120 ò g

60 WNIGGILTTIGCIGTMIWLLSCPPYEHQKRLSLLFVSAVLEGASVGPLIKVAIDVDPSIL 119 121 FGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFF 180 120 ITAFVGTAIAFVCFSAAAMLARREYLYLGGLLSSGLSMLMWLQFASSIFGGSASIFKFE g g ò

181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIIMLKNASEKE 240 ò g

240 EKKKKRRN 247 241 EKKKKRRN 248 ð

RESULT 2 342069 TEGT protein - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

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Gaps

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A85197
TEGT protein homolog [imported] - Arabidopsis thaliana
TEGT protein homolog [imported] - Arabidopsis thaliana
(s)Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: A85197
A;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colc Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A85107
A;Accession: A85107
A;Accession: A85107
A;Accession: A85108
A;Accession: A85108
C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 LYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIBKAHLG 206
                                                                                                                                                                                                                                                                                                                               147 LYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLG 206
                                                                                                                                                                                                                                                                                                                                                                                        87 EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREY 146
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                                                   Indels
Pred. No. 1.9e-35;
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61.7%; Pred. No. 1.9e-35;
cive 22; Mismatches 37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 DMDYVQHSFTFFTDFASLFVQILVLNMLIILEKK 247
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A,Cross-references: GDB:378256; OMIN:600748
A,Map Dostion: 12q12-12q13
C;Superfamily: human testicular protein TEGT
Best Local Similarity 61.7%; Pr
Matches 95; Conservative 22;
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Best Local Similarity (
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A;Map position:
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A;Molecule type: mRNA
A;Cross-references EMBL:X75855; NID:9456206; PIDN:CAA53470.1; PID:9456207
B;Malter, L.; Dirks, B.; Rothermel, E.; Heyens, M.; Szpirer, C.; Levan, G.; Gunther, E.
R;Malter, L.; Dirks, B.; Rothermel, E.; Heyens, M.; Szpirer, C.; Levan, G.; Gunther, E.
A;Molecule to a novel, conserved gene of the rat that is developmentally regulated in the tes
A;Reference number: I57015
A;Accession: I57015
A;Accession: I77015
A;Accession: Jose ARES
A;Access
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C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 11-Jan-2002
C;Accession: E71445
C;Accession: E71445
C;Bergkamp, R.; Dirk
R;Bevan, M.; Bancroff, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
R;Bevan, M.; Wadler, E.; Wambutt, E.; Peitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Augr, S.; Silvey, M.; James, K.; Montfort, A.; Pons, A.; Pungdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C; Chalwatzis, N.
A;Reference mumber: A71400; MUID:98121113; PMID:9461215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:X75856; NID:g456208; PIDN:CAA53471.1; PID:g456209; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 VWLLSAPPYQ - EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:Z97343; NID:g2245073; PID:g2245116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.1%; Pred. No. 3.9e-36;
Matches 100; Conservative 52; Mismatches 72.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                   R;Guenther, E.
submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.1%; Score 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: tegt
C;Superfamily: human testicular protein TEGT
          S42069; I57015; I76675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Map position: 4COP9-4G3845
                                                                                                                                                     Reference number: $42069
Accession: $42069
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A;Accession: D85624
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-219
A;Tessidues: 1-219
A;Cross-references: GB:AE005174; NID:g12514158; PIDN:AAG55456.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000007; PIDN:BAB34477.1; PID:g13360514; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GGTALVFFCCS-AYVLTTRKDMSFLGGMLMAGIVVVLLIGMVANIFLQLPALHLAIS--- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:::| :::| :::| |::| | |::| | |::| | |::| |::| |::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 TTMACMGSMVWLLSAPPYQEQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGAF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 VGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLF------WLHFASSIFGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 SMAVFKRELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AVF-----ILISSGAILFETSNII---HGGETNYIRATVSLYVSLYNIFVSLLSIL 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 SASRNRWSYDSLKNFRQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLL 67
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                                                   A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SSSHDRTS------LLSTHKVLRNTYFLLSLTLAFSAITATASTVLMLPSPGLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 157.5; DB 2; Length 219; 26.7%; Pred. No. 5.9e-07; ive 45; Mismatches 80; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 219;
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12.4%; Score 157.5; DB 2;
Best Local Similarity 26.7%; Pred. No. 5.9e-07;
Matches 64; Conservative 45; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: yccA
C,Superfamily: Escherichia coli ybhL protein
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les 64; Conservative
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A,Gene: ECs1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein STY1112 [imported] - Salmonella enterica subsp. enterica servov Typhi (;Species: Salmonella enterica subsp. enterica servova Typhi d;Note: this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002 C;Accession: Alfo£28 C;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable carrier/transport protein yccA [imported] - Escherichia coli (strain 0157:H7, s C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Aug-2002
C;Accession: D85624
R;Perna, NT:; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose; D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, iller, L.;
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A;Cross-references: GB:AL513382; PIDN:CAD08212.1; PID:g16502260; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 PPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFDPSIVFG-AFVGCAVVFGCFSAAA 138
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                                                                                                                                                                                                                                                                                                                                                                                        77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWIMATPHSHETEOKRIGILAGRAFLTGVGLGPALERCIAVNPSILPTAFMGTAMIFTCF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                            Gaps
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                                                                                                                                                                                                                                                       19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI --GGLLTTWACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 RQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLLTTMACMGSMVWLL$A 82
                                                                                                       7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 DTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | |:::| | | |::|:: ::|: ISSGAILYETSNII---HGGETNYIRATVSLYVSLYNIFVSLLSIL 213
     DB 2;
37.1%; Score 471.5; DB 2;
42.2%; Pred. No. 1.9e-35;
ive 51; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9e-08;
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29.2%; Pred. No. 3.9e
tive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: STY1112
C,Superfamily: Escherichia coli ybhL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.2<sup>3</sup>
Matches 66, Conservative
                                                                                            98; Conservative
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                        Local
     Query Mat
Best Loca
Matches
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Accession: 113. Address. M.A.; Barrell, B.G.; Murphy, L.; Harris, D. Submitted to the EMBL Data Library, September 1998

Submitted to the EMBL Data Library, September 1998

A; Reference number: 221954

A; Reference number: 221954

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-26 < WOO>

A; Cross-references: EMBL:AL031798; PIDN:CAA21183.1; GSPDB:GN00068; SPDB:SPCC576.04

A; Experimental source: strain 972h-; cosmid c576

A; Genetics: SPDB:SPCC576.04

A; Map position: 3
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C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 29-Oct-1999 #text_change 29-Oct-1999
C,Accession: T34438
R,Bradshaw, H.
B,Description: The sequence of C. elegans cosmid KILH12.
A,Reference number: 221526
A,Reference number: 221526
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Residues: 1-342 eBRA>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 FWL----HFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGVLGAVFAPLCFMA---GPVLTRAAWYTAGIV-GGLSATAITAPSEKFLMMSGPLAMGF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LWN------IGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SQSASRNRWSYDSLKNFRQISPLVQ-----THLKQVYLTLCCAL-VASAAGA--YLHI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 NESATEN----PAVDOFKNTTPVAECAKSIRMAFLRKVYAILTAQLFVTSLFGGIFYLHP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTLCCALVASAAGAYLHILWNIGGLLTTMACMGSWWL-LSAPPYQEQKRVALLMAAAL- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 144; DB 2; Length 266; 24.9%; Pred. No. 1.2e-05; Indels iive 39; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.3%; Score 143.5; DB 2; Best Local Similarity 23.7%; Pred. No. 1.8e-05; Matches 51; Conservative 47; Mismatches 86;
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A;Map position: 4
A;Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFTDFGAVFVRILII--MLKN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYLDFINLFIRILQILGMLON 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
          C; Accession: T41414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches 6
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A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-219 <BLAT>
:Cross-references: GB:AE000199; GB:U00096; NID:g1787202; PIDN:AAC74056.1; PID:g1787205;
Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                    C;Species: Escherichia Goli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: S07180; #s64818
R;Tamura, F;; Nishimura, S;; Ohki, M.
EMEO J; 3, 1100-1107, 1984
A;Title: The E. coli divE mutation, which differentially inhibits synthesis of certain A;Reference number: S07180; MUID:84236106; PMID:6376117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable receptor-associated protein - fission yeast (Schizosacchardmydes bombe)
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 LGGTALVFFCCS-AYVLTTRKDMSFLGGMLMAGIVVVLIGMVANIFLQLPALHLAIS--- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TTMACMGSMVWLLSAPPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 FVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLF-------WLHFASSIFG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 GSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVKILII 231
--AVF-----ILISSGAILFETSNII---HGGETNYIRATVSLYVSLYNIFVSLLSIL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTLAFSAITATASTVLMLPSPGLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Status: translation not shown
A/NOLecule type: DNA
A/Residues: 1-219 < TAM>
A/Cross-references: EMBL:X00547; NID:g41283; PIDN:CAA25218.1; PID:g41284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 ---AVF-----ILISSGAILFETSNII---HGGETNYIRATVSLYVSLYNIFVSLLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
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                                                                                                                                                                                                                                      probable glutamate receptor yccA - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A64838
Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: The complete genome sequence of Escherichia coli K-12. Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77; Indels
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12.4%; Score 157.5; DB 2
Best Local Similarity 27.0%; Pred. No. 5.9e-07;
Matches 65; Conservative 46; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
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integral membrane protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: O1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AB3484
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliter A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:AE008917; PIDN:AAL53040.1; PID:g17983899; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 RIQSLSVGTAQAIFWGYAALVGLSL---SSIFIVFTGQSIVRTFFVTAASFGALSLYGY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AYLHILWN---IGGLLTTWACMGSMVWLLSAPPYQE-----QKRVALLMA--AALF---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 -----LGGLLSSGVSLLFWLHFAS--SIFGGSMAVFKFELYFGLLVFVGYIVFDTQE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YD--RDYTQDSRLPGTFSSRVYGWMTAGLAVTALTSLGLYATGAYRTLFSLW----WVWC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 --EGASIG------PLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 136.5; DB 2; Length 245; 29.1%; Pred. No. 5.3e-05; Live 31; Mismatches 76; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 IIEKAHLGD-----MDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 | | : | | : | | | | | | 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Gene: BMEI1859
A.Map position: I
C.Superfamily: Escherichia coli ybhL protein
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Matches 64; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: AE3484
A,Status: preliminary
A,Molecule type: DNA
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A; Status: preliminary
A; Molecule type: DNA
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A;Residues: 1-297 <MAU>
A;Cross-references: EMBL:271581; NID:g1302402; PID:e239757; PID:g1302403; MIPS:YNL305c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying C, and a novel putative serine/threonine protein kinase gene. R60394; MUD:96132033; PMID:8553702
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                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YNL305c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0405
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence revision
C;Accession: S63281; 860395; 86127
C;Accession: CT.C.; Urbanus, J.H.M.; Planta, R.J.
Submitted to the Protein Sequence Database, April 1996
A;Reference number: S63266
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241 GVVPVANIGAFFLPPGSALGASLA--SIVVYGGLILFSAFLLYDTQRLVXKAENHPHSSQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: U23084; NID: g1050853; PID: g1050855
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                                                                                                                   -----HLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                 LYGSDMQIRSFDPINAQMSIYMDVLNIFMRLVMIM 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain S288C
R;Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.
Yeast 11, 1303-1310, 1995
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Submitted to the EMBL Data Library, March 1995
A;Reference number: S66127
A;Accession: S66127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 VKHALTLFTDFGAVFVRILLIMLKNASE 238
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A;Molecule type: DNA
A;Residuss: 1.-297,'D' <MAN>
A;Cross-references: EMBL:U23084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keywords: transmembrane protein
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Residues: 1-297 <MAF>
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R,Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic, Acids Res. 28, 1397-1466, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002287; GB:AE002160; NID:g7190237; PIDN:AAF39078.1; PID:g7190;
A;Experimental source: strain Nigg (MoPn)
conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg) C;5pecies: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;5pecies: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C;Accession: B81729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 130.5; DB 2 27.2%; Pred. No. 0.00018; tive 35; Mismatches 95
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Scatus: preliminary
;Motecule type: DNA
;Residues: 1-238 <ARN>
;Cross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68416.1; PID:g332928
;Gross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68416.1; PID:g332928
;Gross-references: serotype D, strain UM-3/Cx
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70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                                                      AFVGCAVVFGCFSAAAMLAR, -----RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMA 175
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10.1%; Score 128.5; DB 2; Length 238;
Best Local Similarity 25.9%; Pred. No. 0.00028;
Matches 63; Conservative 38; Mismatches 95; Indels 47;
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C;Superfamily: Bscherichia coli ybhi protein
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GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on:

May 25, 2003, 11:26:54; Search time 36 Seconds (without alignments) 285.726 Million cell updates/sec

US-09-955-526-4 1272 1 MEGFISFFDSQSASRNRWSY......LIIMLKNASEKEEKKKKRRN 248 Title: Perfect score: Sequence:

112892 segs, 41476328 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

112892 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	*	arabidopsis	Oryza	homod	para	rattus norv	dros		esch																homod		rickette	candida al	bacillus	cavia porce	lactoo	streptococc		
	Description	Q91d45	gempda gembda	P55061	09ia79	P55062	Q9veh3	Q9h3k2	P06967	P48558	Q9pla1	084826	Gacum5	09rvx8	99piq8	P75768	P09723	003268	Q9da39	058916	P44477	Q9jri0	Q9ksa1	025578	Q9hc24	Q9zkt1	Q9ze15	074713	P27611	035899	09ceu8	Q9a1b9	P48994	P72060
SOMMAKIES	Q	BI1 ARATH	BI1_ORYSA	BI1 HUMAN	BI1 PAROL	BI1 RAT	BI1_DROME	GHIT HUMAN	YCCA_ECOLI		Y206_CHLMU	Y819 CHLTR	Y402_PASMU	Y893 DEIRA	Y236 CAMJE	YBHL_ECOLI	US21_HCMVA	YQ04_PSEAE	ZPRO_MOUSE	YF21 METJA	YCCA_HAEIN	Y420 NEIMA	YD58_VIBCH	Y920_HELPY	ZPRO_HUMAN		Y147_RICPR	HGT1_CANAL	NHAC_BACFI	S6A4_CAVPO		Y358_STRPY	TRPL DROME	EMBA_MYCTU
	DB	-	Н	Н	-	٦	Ч	٦	Н	٦	Н		-	ч	٦	н	-	-	-	-	Н	-	Н	Н	H	-	-4	Н	н	~	ч	Н	н	-
	Length	247	249	237	237	236	245	345	219	297	238	238	220	231	231	234	239	222	238	422	220	227	223	230	238	230	236	545	462	630	234	229	1124	1094
9/0	Query Match	o.	ω.	۲.		۲.	4.	۳.	ď	ä	٥.	٥.				9.0			•			•	•	8	٠	٠	•	•		•	•	•	•	
	Score	1023.5	876.5	481.5	481.5	479	312	165	157.5	143	130.5	128.5	125.5	124	123.5	122	121.5	120	120	120	114.5	114	113	112.5	111	109.5	108.5	97	95	93.5	93	92.5	91	06
	Result No.	Н	7	m	4	ហ	9	7	80	თ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	36	27	28	50	Θ.	31	32	33

Q9a2a3 caulobacter Q47479 loligo blee Q9cdm7 lactrosocous Q29470 archaeoglob Q9evn4 pseudomonas G1499 borrelia bu P4762 mycoplasma P28008 staphylococ Q9519 polypterus P1945 pseudomonas P1944 haemophilus Q18864 caenorhabdi
YOG3 CAUCR NUIM_LOLBL YOR LACLA YOR ARCTU RNFD_PSEST RNFD_PSEST Y320_MYCGE PTMB_STACA NUGM_POLOR NUSY_PSEST FTSW_HAEIN SUR4_CAEEL
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ALIGNMENTS

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POTENTIAL.
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MEDLINE=96015061; PubMed=8530040;
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MEDLINE=98325348; PubMed=9660918;
Xu Q., Reed J.C.;
          59 PO
85
113 PO
139 PO
231 PO
27114 MW;
                                                                                                                           66.3%;
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                                                                                                                                      Conservative
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            39
65
93
119
151
213
249 AA;
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EEKKRKKRS 249
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                   EEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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 Apoptosis;
TRANSMEM
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Matches 165;
                                               TRANSMEM
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                                                                                                            Query Match
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                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 WNIGGILTTIGCIGTWIWLLSCPPYEHQKRLSLLFVSAVLEGASVGPLIKVAIDVDPSIL 119
                                                                                                                                                                                                                                                                121 FGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                  LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240
                                                                                                                                                                                                                                                                                                                                 180 LYFGLLIFVGYMVVDTQEIIEKAHLGDMDYVKHSLTLFTDFVAVFVRILIIMLKNSADKE 239
                                                                                                                                                                                                               WNIGGLLTTWACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                      Gaps
                                                                                                                                                              1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                             Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                       120 ITAFVGTAIAFVCFSAAAMLARRREYLYLGGLLSSGLSMLMWLQFASSIFGGSASIFKFE
                                                                                                                                       ä
                                                                                                             80.5%; Score 1023.5; DB 1; Length 247;
                                                                                                                                      24; Indels
                                                                                     FD3AAEA713363945 CRC64;
                                                                                                                       ; Fred. No. 1.3e-69; 31; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bax inhibitor-1 (BI-1) (OSBI-1).
                     POTENTIAL.
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InterPro.; IPRO02199; Bax inhbtrl.
Pfan; PF01027; UPF0005; I.
PROSITE; PS01243; BII; 1.
                                                                                     27483 MW;
                                                                                                                           77.48;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
 Transmembrane
                       112
138
165
193
232
                     92
118
145
173 * 1
212
247 AA;
                                                                                                                          Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                   EKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                          240 EKKKKRRN 247
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Apoptosis;
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RESULT 2 BII_ORYSA

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61 LNIGGMLTWLGCVGSIAWLFSVPVFEERKRFGILLAAALLEGASVGFLIKLAVDFDSSIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEK- 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 WNIGGLLTTMACMGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
                                                                                                                                                                                                                                                                                                                                                                       121 FGAFVGCAVVFGCFSAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFE 180
                                                                                                                                                                                          1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                  68.9%; Score 876.5; DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter L., Marynen P., Szpirer J., Levan G., Guenther E., "Identification of a novel conserved human gene, TEGT.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BII HUMAN STANDARD; PRT; 237 AA. PS55061, 014938; Q96550, 01-0CT-1996 (Rel. 34, Created) 15-UTN-2002 (Rel. 41, Last sequence update) 15-UTN-2002 (Rel. 41, Last annotation update) Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript). BII OR TEGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Cowling R.T., Birnboim H.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
FEAE334173F6D384 CRC64;
                                                                                                        43;
                                                                            Pred. No. 1.1e-58;
40; Mismatches 43
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 IWLWATPHSHETEQKRLGLLAGFAFLTGVGLGPALEFCIAVNPSILPTAFMGTAMIFTCF 128
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee J., Jeon J., Song Y.;
"Liver cDNA from Japanese flounder with similarity to TEGT.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Taleostai, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes,
Pleuronectoidei, Paralichthyidae, Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 SAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKEEKKKKR 246
                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> P (IN REF. 1).
-> V (IN REF. 1).
6567E73A1AD6238E CRC64;
!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
!- SIMILARITY: BELONGS TO THE BII FAMILY.
                                                                                                                                                                                                                                                                                                                                                          37.9%; Score 481.5; DB 1
42.7%; Pred. No. 2.7e-29;
tive 52; Mismatches 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Paralichthys olivaceus (Flounder).
                                                                                                                                                                                   InterPro; IPR002199; Bax inhbtr1. Pfam; PF01027; UPF0005; \overline{1}. PROSITE; PS01243; BI1; 1.
                                                                                                                         EMBL; X75861; CAA53472.1; -.
EMBL; AR033053; AA887479.1; -.
EMBL; BC000316; AAB100316.1; -.
Genew; HGNC:11723; IEGT.
                                                                                                                                                                                                                                                                                                                                     26537 MW;
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                                                                                                                                                                                                                     Transmembrane
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                                                                                                                                                                                                                                                                                                              169 1
187 1
237 AA;
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                              Genew; HGNC:
MIM; 600748;
                                                                                                                                                                                                                    Apoptosis; 1
TRANSMEM
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Q91A79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 VWLLSAP--PYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 SAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 NFDSLFKFSQISHSTQVHLKAVVSSLAVCMFVAAAGSYVHVVTRLFQGGMLSVLGSLGWM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley, TISSUE=Testis;
MEDLINE=94281747; PubMed=8012111;
Malter L., Dirks B., Rothermel E., Heyens M., Szpirer C., Levan G.,
Guenther E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamm. Genome 5:216-221(1994).
-!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
-!- SUBCEDILIULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
-!- SIMILARITY: BELONGS TO THE BI1 PAMILY.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
-!- SIMILARITY: BELONGS TO THE BIL PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.9%; Score 481.5; DB 1; Length 237; 41.3%; Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 DTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIL RAT STANDARD; PRT; 236 AA.

855062; Q64712;
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
BIL OR TEGT.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQLIEKAENGDKDYVWHSVDLFLDFITIFRKLMVILALNDKDKKKEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Mismatches
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InterPror; IPRO02199; Bax inhbtrl.
Pfam; PF01027; UPP0005; I
PROSITE; PS01243; B11; 1.
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73
107
133
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193
26570 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; Transmembrane
TRANSMEM 30 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sukaryotea, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda, Insecta, Pterygote, Neopera: Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNI--GGLLTTMACMGSM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 VWLLSAPPYQ--BOKRVALLMAAALFEGASIGPLIBLGINFDPSIVFGAFVGCAVVFGCF
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable Bax inhibitor-1 (BI-1).
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Pfam; PF01027; UPF0005; I.
PROSITE; PS01243; BI1; 1.
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Matches 100; Conservative 5
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166
206
236 AA;
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89 ----KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 REYLYLGGILSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIBKA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Score 312; DB 1; Length 245; 34.4%; Pred. No. 1.2e-16; ive 48; Mismatches 83; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57ACD341C5C94720 CRC64;
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InterPro; IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; 1.
PROSITE; PS01243; B11; 1.
Apoptosis; Transmembrane.
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76
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27574 MW;
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Best Local Similarity 34.44
Matches 77; Conservative
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                                     GHIT HUMAN STANDARD; PRI; 345 AA.
99H3Z; 09S894; O9H0P2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Growth hormone inducible transmembrane protein (Dermal papilla derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bake In the
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Urinary bladder;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Fotential).
-!- SUBLEARITY: BELONGS TO THE BII FAMILY.
                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Dermal papilla,
Tikeda A., Yamashita M., Yoshimoto M.;
"Molecular cloning of a dermal papilla derived gene.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   Z.M., Li Y., Huang Y.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  R.A.;
to the EMBL/GenBank/DDBJ databases
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InterPro; IPR002199; Bax inhbtr1.
Pfam; PF01027; UPF0005; 1.
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EMBL, AF111820, AAD20052.1, --
EMBL, AF060923, AAG43135.1, --
EMBL, AL136713, CAB66648.1, --
EMBL, BC010354, AAH10354.1, --
                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
Mei G., Yu W., Gibbs R.
Submitted (FEB-1999) to
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146
180
211
234
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Submitted (APR-1998)
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               88 Q---KRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARRR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 EYLYLGGILSSGVSLLFWLHFASSIFGGSM-----AVFKFELYFGLLVFVGYIVF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86; Indels 38; Gaps
                                                                                                                                                                                                                                                                                      36 HLKQVYLTLCCALVASAAGAYLH--1LWNI----GGLLT---TMACMGSMVWLLSAPPYQE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-842256.06; PubMed-6376117;
Tamura F., Nishimura S., Ohki M.;
Tamura F. Oli dive mutation, which differentially inhibits synthesis
of certain proteins, is in tRNASerl.";
EMBO J. 3:1103-1107(1984).
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SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Roch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bscherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQEIIEKAHLGDM-----DYVKHALTLFIDFGAVFVRILIIMLKNASEKE 240
                                                                                                                                                                                            Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
245 265 POTENTIAL.

72 292 POTENTIAL.

4 4 A -V (IN REF. 4).

64 64 E -> G (IN REF. 3).

74 74 1-> M (IN REF. 4).

118 118 Q -> M (IN REF. 4).

345 AA, 37205 MW, 808FAED86A9CD98E CRC64;
                                                                                                                                                                                          13.0%; Score 165; DB 1; 26.3%; Pred. No. 1.4e-05; ative 47; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ul-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yccA.
                                                                                                                                                                                                                                            61; Conservative
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                                                                                                                                                                                                                Local Similarity
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Local Similarity 24.3
nes 65; Conservative
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           124 FVGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLF-------WLHFASSIFG 171
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                       12 SASRNRWSYDSLKNFRQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
STRAIN=S9132031, PubMed=8553702;
MAUTER K.C.T., Urbanus J.H.M., Planta R.J.;
"Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
SIMILARITY: BELONGS TO THE BIL FAMILY. STRONG, TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SSSHDRTS-----LISTHKVLRNTYFLLSLTLAFSAITATASTVLMLPSPGLI
                                                                                                                                                                                                                                                                                                                                                                                                 68 TIMACMGSMVWLLSAPPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GSMAVFKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBG-1998 (Rel. 37, Last annotation update)
Hypothetical 33.6 KDa protein in MCKI-RPS19B intergenic region.
YML305C OR N0405.
                                                                                                                                                                                                                                                                                                             DB 1; Length 219;
                                                                                                                                                                                                                                                                                                                                  77; Indels
                                                                                                                                                                                                     Transmembrane, Complete proteome. POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                              POTENTIAL.
4F787B853042ACD8 CRC64;
                                                                                                                                                                                                                                                                                                            12.4%; Score 157.5; DB 1
27.0%; Pred. No. 3.4e-05;
iive 46; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 AA
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                                                                                                               EMBL; X00547; CAA25218.1; -.
EMBL; AE00199; AAC74056.1; -.
EMBL; D90734; BAA35735.1; -.
PIR, S77180; S07180.
ECGGENE; EG11113; YCCA.
INTERPYO; IPR00219; BAX_inhbtr1.
Pfam; PF01027; UPF0055; I.
PROSITE; PS01243; B11; 1.
                                                                                                                                                                                                                                                                                         23362 MW;
                                                                                                                                                                                                                                                                                                                                   65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                          134
158
196
219 AA;
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                                                                                                                                                                                                     Hypothetical I
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P48558;
          HI0044
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213 L 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 CLS-LVTLA--YDKDTVLSALLITTIVVVGVSLTALSER-----FENVLNSATSIYYWL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 MVWLLSAP-----VALLMAAALFEGA 103
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STRAIN=MOPD / Nigg;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and rovel puttative serine/threonine protein kinase gene.";
Yeast 11:1309-1310(1995).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PLV-QTHLKQVYLTLCCALVASAAGAY------LHI-LWNIGGLLTTMACMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 -IWLAVSPRPEDYEASVPEPLLIGSSEEPAQEQRRLPWYVLSSYKQKLTLLSIFTLSEAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 SIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 HF------ASSIFGGSMAVFKFELYFGLL---VFVGYIVFDTQEIIEKAHLGDMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 NWGLWIMIGMGLTALLFGWNTHSSKFNLLYGWLGAILFTAYLFIDTQLIFRKVY--PDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 143; DB 1; Length 297; 24.3%; Pred. No. 0.00053; ive 44; Mismatches 83; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330784DA17152BB0 CRC64;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TC0206.
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POTENTIAL.
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POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U23084; AAC49093.1; -.
EMBL; Z71881; CAA96233.1; -.
EQD; S0005249; YNL305C.
InterPro; IPR00199; Bax inhbtr1.
Pfam; PF01027; UPF0005; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 VPKPELYFGLLVFVGYIVFDTQEIIEKAHL----GDMDY---VKHALTLFTDFGAVFVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 FÁTLGVSFYIQAQIQKLSVPAV----MGLFLÁYSILEGMFFGTLVPVYAAQFGGGVVWA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 YD--RDYAQDSRLPGTFSSRVYGWMTAGLAVTALTSLGLYATGAYRALFPMW-----WIWC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 YDSLKNFRQISPLVQTHLKQVY-----LTLCCALVASAAGAY--LHILWNIGGLLTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                         "Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
                                                                              Chlamydia trachomatis.";
Science 282:778(1999)
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE BII FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%; Score 128.5; DB 1; Length 238; 25.9%; Pred. No. 0.0052; Live 38; Mismatches 95; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Complete proteome
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Last annotation update)
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InterPro; IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; 1.
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69
98
125
101
161
186
228
PO
264 MW;
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hes 63; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEJ cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email, to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 MACMG-----SMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 FATLGVSFYIQAQIQKLSVPAV----MGLFLAYSVLEGMFFGTMVPVYAAQFGGGIVWA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AFVGCAVVFGCFSAAAMLAR-----RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Gaps
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Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
Eisen J., Fraser C.M.;
                                                                                                                                              Nucleic Acids Res. 28:1397-1406(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE BI1 FAMILY.
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                                                                           "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein CT819.
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TIGR; TC0206; -.
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                                                                                                                    pneumoniae AR39.";
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NCBI_TaxID=197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 RREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQEIIEK 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 286:1571-1577(1999).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE BII FAMILY.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                              Transmembrane; Cc
POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                EMBL, AE006076, AAX02486.1; -.
InterPro, IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23936 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53, Conservative
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70
94
125
155
216
                                                                                                                                                                                                                                                                                                Hypothetical protein;
TRANSMEM 25 4
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Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 MACMGSMVWILSAPPYQEQKRVALLMAAALFEG-ASIGPLI--ELGINFDPSIVFGAFVG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 MLAQLALVFVLS----MFAQRLSAAVAGALFVGYAALTGLTFSALLFAYSPAAVITAFAV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 LKNFRQISPLVQTHLKQV-----YLTLCCALVASAAGAYL-----HILWNIGGL-LTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VKSMQQIAMTQQKTLDQVRTFMARTYSWMAAGLALTAGVAYLTAQNEGLAMQVASLRLPL 61
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LYFGLLVFVGYIVFDTQEIIEKAHLG-----DMDYVKHALTLFTDFGAVFVRILII 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 124; DB 1; Length 231;
Pred. No. 0.011;
1; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24447 MW; BBB7D76A6445D9C9 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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41; Mismatches
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Pfam; PF01027; UPF0005; I.
                                                                                                                                                                                                                                                                            EMBL; AE001942; AAF10471.1; -.
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nes 62; Conservative
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STRAIN=NCTC 11168;
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Oshima T., Alba H., Baba T., Fulita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kailhara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito, M.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AVVFGCFSAAAMLARRREYLYLGG-----LLSSGVSLLFWLHFASSIFGGSMAVFKFELY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 SMVWLLSAPPYQEQKRVALLMAAALF----EGASIGPLI--ELGINFDPSIVFGAFVGC 127
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              8 YSRSKEFENTRSSELSIFIKÓTYQLFAASLLAATVGAYVGIFALASFFIQSQVTFWILFA 67
                                                                                                                                                                                                                                                                                                                                                                                                             20 YDSLKNFRQI-SPLVQTHLKQVYLTLCCALVASAAGAYLHIL----WNIGGLLTTWACMG 74
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SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Griedy M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                       9.7%; Score 123.5; DB 1; Length 231; 26.8%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 FGLLVFVGYIVFDTQEIIEKAHLGDMDY-VKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.012;
38; Mismatches 100; Indels
                                                                                                                                                                                                Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                   POTENTIAL.
279E67CA380336C9 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ybhi.
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                                                                                                                         EMBL; AL139074, CAB72705.1; -.
InterPro; 187802199; Bax inhbrr1.
Pfam; PF01027; UPF0006; I.
Hypothetical protein; Transmembrar TRANSMEM 36 56 POTEI
                                                                                                                                                                                                               56 PO
78 PO
103 PO
163 PO
190 PO
25487 MW;
                                                                                                                                                                                                                                                                                                                                                      Similarity 26.8%
62; Conservative
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ID YBHL_ECOLI
AC P75768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 VWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 LQTYMAQVYGWMTVGLLLTAFVAWYAANSAAVMELLFTNRVFLIGLIIAQLALVIVLSAM 76
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
-!- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 VGYIVFDTQEII----EKAHLGDMDYVKH-----ALTLFTDFGAVFVRILLI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 122; DB 1; Length 234; 25.5%; Pred. No. 0.016; tive 41; Mismatches 81; Indels
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Job time : 39 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90716; BAA3544.1; -- Cocosen, E01368; ybh. LinterPro; IPR00199; Bax inbtrl. Pfam; PF01027; UPF0005; T.
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123
157
184
227
25902 MW;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica napus (Rape), and
Brassica oleracea (Cauliflower).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708, 3712;
                                                                                                                             ELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNASEK 239
                                                                                                                                                                                            240
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SPECIES-B.O.Deracea,
Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
"The isolation and characterization of broccoll homologs to
Arabidopsis PCD genes, LSD1 and BI: their role during cell death and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolduc N., Brisson L., "Characterization of Bax inhibitor 1 from Brassica napus."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF30555; AAK73101.1; -.
EMBL; AF453320; AAL50791.1; -.
EMBL; AF453320; AAL50791.1; -.
InterPro; IPR00119; Bax_inhbtr1.
InterPro; IPR0011064; Crystallin.
PFam; PF01027; UPF0005; 1.
PROSITE; P801243; B11; UNKNOWN 1.
PROSITE; P801224; CRYSTALLIN BETAGAMMA; UNKNOWN 1.
SEQUENCE 247 AA; 27526 WW; F5A5B5EFF6D4E8DB_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ol-war-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Bax inhibitor 1 (Bax inhibitor-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES-B.napus; STRAIN-CV. WESTAR; TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                      241 EEKKKKRRN 249
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Submitted (NC
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61 WNIGGLITTWACMGSWVWLLSAPPYOEOKRVALLMAAALFEGASIGPLIELGINFDPSIV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 WNIGGILTTIACCGTWIWLLSCPPYEQQKRLSLLFLSAVLEGASVGPLIKVAVDPDFSIL 119
                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TAXID=3712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. MESFSSFFDSQPGSRS-WSYESLKNLHQISPSVQNHLKRVYLTLCCALVASAFGAXLHVL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEGFTSFFDSQSASRNRWSYDSLKNFRQISPLVQTHIKQVYLTLCCALVASAAGAYLHIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                  Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.; "The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSD1 and B1: their role during cell death an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILLIMLKNASEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  senescence.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001299; Bax inhbrr1.
InterPro; IPR001064; Crystallin.
Pfan; PF01027; UPF0005; 1.
PR0STITE; PS01243; B11; UNKNOWN 1.
PROSTITE; PS01255; CRKSTALLIN BETAGAMMA; UNKNOWN 1.
SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E CRC64;
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Last annotation update)
                                                                                         Last sequence update)
Last annotation update)
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      246 AA
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                                                               Created)
                                                                                                                                                                                                            Brassica oleracea (Cauliflower).
                                                            01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, Bax inhibitor-like protein.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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Matches 187; Conservative
PRELIMINARY;
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Matches
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MEDLINE=21085660; PubMed=11217881;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Narchionni L., Mashima J., Mazzarelli J., Mombarts P.M., J.,

Lyons P., Narchionni L., Mashima J., Mazzarelli J., Mowdone P., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huckelhoven R., Dechert C., Trujillo M., Kogel K.H.;
Huckelhoven R., Dechert C., Trujillo M., Kogel K.H.;
"Expression analysis of putative cell death regulator genes in near-
isogenic, resistent and susceptible barley lines inoculated with the
powdery mildew fungus.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ290421; CAC37797.1; -.
InterPro; IPR002199; Bax inhbrr1.
Pfam; PF01027; UPF0005; 1.
SEQUENCE 247 AA; 26962 MM; 4DBDEPIEFAE22CC4 CRC64;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        SFFDSQSASRNRWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGG 65
                                                                                                                                                                                                                                                                                                                                     3 AFYSTSSAAASGWGHDSLKNFRQISPAVQSHLKLVYLTLCFALASSAVGAYLHIALNIGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 GTAIAFGCFSGAAIIAKRREYLYLGGLLSSGLSILLMLQFVTSIFGHSSGSFMFEVYFGL
                                                                                                                                                                                                                                                                                                                                                                                                                               126 GCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLFWLHFASSIFGGSMAVFKFELYFGL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                             Length 247;
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                Hueckelhoven R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
5031406905Rik protein (RIKEN cDNA 5031406P05 gene).
                                                                                                                                                                                                                                           69.4%; Score 883; DB 10; 67.8%; Pred. No. 7.1e-70; live 36; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                         SEQUENCE FROM N.A.
STRAIN-CV. PALLAS; TISSUE-LEAF;
STRAIN=CV. PALLAS; TISSUE=LEAF;
                                                                                                                                                                                                                                                                          Matches 164; Conservative
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243 RK 244
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Best Local
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SEQUENCE FROM N.A.

MEDLINE=99121113; PubMed=9461215;

MEDLINE=99121113; PubMed=9461215;

MEDLINE=99121113; PubMed=9461215;

BergAmp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,

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Ridley P., Hudgon S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

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Andler E., Wandhutt R., De Clerck R., van Montagu M., Lecharny A.,

Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

Raborg S., Gy I., Kreis M., Pank B., Mueller-Auer S.,

Silvey M., James R., Montfort A., Pons A., Pujddomenech P., Douka A.,

Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

Noukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

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Belseny M., Voet M., Volckart G., Mewes H.W., Klosterman S.,

Analysis of I.9 Mb of contiguous sequence from chromosome 4 of

Nature 391:485-488(1998).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaces, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 VWILSAPPYQ -- EOKRVALLMAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCF 134
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Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%; Score 490.5; DB 11; Length 237; 43.1%; Pred. No. 2.1e-35; Live 52; Mismatches 73; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 DIQLIIEKABHGDKDYIWHCVDLFLDFVTLFRKIMLILAFN--EKDKKKEKK 237
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                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (ARF-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO19865; BAB31892.1; -.
EMBL; BCO05888; ARHO5888.1; -.
MGD; MGI:1915559; 5031406P05Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002199; Bax inhbril.
InterPro; IPR001064; Crystallin.
Pfam; PF01027; UPF0005; 1.
PROSITE; PS01243; B11; UNKNOWN 1.
PROSITE; PS0125; CRYSTALLIN BETAGAMMA; UNKNOWN 1.
SEQUENCE 237 AA; 26477 NW; 788BGEE7EB34AFFC CRC64;
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U-JAN-1999 (TrEMBLrel. 10, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 29.3 kDa protein (TEGT protein homolog)
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                                                                                                                                                                      Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Query Match
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                                                             RESULT 8
Q9VIB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Make of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSGVSLLFWL----HFASSIFGGSMAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 FKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIMLKNA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 LYHGASLACCMSILWWVQIASSIFGGSTTVVKFELYFGLLIFVGYIVVDTQMITEKAHHG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=COLUMBIA;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 5. XI.";
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                                                                                                                                                                                                                                                                                                                                                Length 262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural analysis of Arabidopsis thaliana chromosome Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AB025609; BA4981081.; InterPro; IPR002199; Bax inhbr1. Pfam; PF01027; UPP0005; DAPEm; PF01027; UPP00051
                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Z97343; CAB10538.2; -.
                                                                                                                                                             EMBL; AL161546; CAB78761.1; -
INCETPO; IRRO02199; Bax inhbtr1.
Pram; PF01027; UPF0005; 1
PROSITE; PS01243; B11; UNKNOWN 1.
SEQUENCE 262 AA; 29337 MW; 04111E60CE90F24F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Similarity to Bax inhibitor-1.
                                                                                                                                                                                                                                                                                                                                                Match 37.1%; Score 472; DB 10; Local Similarity 61.7%; Pred. No. 9.8e-34; es 95; Conservative 22; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%; Score 435.5; DB 1
ilarity 50.0%; Pred. No. 1.1e-30;
Conservative 32; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 DMDYVQHSFTFFTDFASLFVQILVLNMLIILEKK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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AD-----RIRRN 183
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nes 96; Conserv
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[2]
SEQUENCE FROM N.A.
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Matches
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Q9LTB6
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RX STAINT=EMERKLEY;

RX Addams MD. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA dams MD. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA dams MD. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides R.A., Lewis S.E., Richards S.A. Amburner M., Henderson S.N.,

Sutcon G.G., Mortnan J.R., Yandell M.D., Zhang Q., Chen L.K.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Adriaws-Ffannkoch C.R., Baldwin D.,

RA Ballew R.M., Bencos P.V., Berman B.P., Bhandari D., Bolahakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Cherry J.M., Cawley S., Dahle C., Davenpour L. B., Duries P.,

RA Durbin X.J. Evangelista C.C., Ferraz C., Perriera S., Fleischman W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glabar I., Bouck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marven F., Karpen G.H., Ke Z., Kuni Bon. J.A., Ketchun K.A.,

Alali M., Kalush F., Kalpen G.H., Ke Z., Gubar P., Houck J.,

RA Harris N.L., Martei B., McIntosh T.C., McLeod M.P., McShrefi A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kuni Bon. J.A., Ketchun K.A.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShrefi A.,

RA Harris W.C., Sternicon K.A., Nikon K., Nikon W., Holson D.L.,

RA Bazzolo M., Pittuma G.S., Pan S., Pollard J., Moshrefi A.,

RA Bazzolo M., Pittuma G.S., Pan S., Pollard J., Weissenbach J.,

RA Briekas R., Scalare C.D., Kraft C., Kraf
                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 HLKQVYLTLCCALVASAAGAY----LHILWNIGGLLTTWACM-----GSMVWLLSAPP 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 AA; 32546 MW; 0F25177F36ECA99D CRC64;
                                                                                                           Last sequence update)
Last annotation update)
    305 AA
                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhbtr1.
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FlyBase; FBgn0037506; CG1287.
InterPro; IPR002199; Bax inhb
                                                                      01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.7
Matches 61, Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF01027; UPF0005; SEQUENCE 305 AA: 3254
                                                                                                                                                                                              CG1287 protein.
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FROM N.A.
F2 / SGSC1412 / ATCC 700720;
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                                                                                                                                                                           EMBL, AE008747; AAL20018.1; -. InterPro. 1PR002199; Bax_inhbtrl. Pfam; PF01027; UPF0005; I. PROSITE; PS01243; E11, UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                          67; Conservative
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                                                                                                                                                              413:852-856(2001)
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                              Nature
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                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 EYLYLGGLLSSGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 GFGAKQLAWLVHCAVL-GAVLAPMCLLG----GPILTXALLYTSGIVGALSTVAACAPSE 199
                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheara; Hexapoda, Insecta;
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha,
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GFGAKQLAWLVHCAVL-GAVLAPMCLLG----GPILTKALLYTSGIVGALSTVAACAPSE 259
                                                 145 BYLYLGGLLSSGVSLLF-----WLHFASSIFGGSMAVFKFELYFGLLVFVGYIVFDTQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 HLKQVYLTLCCALVASAAGAY----LHILMNIGGLLTTMACM-----GSMVWLLSAPP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 EIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 RIVKSAELYPQYSKFPYDPINHALAIYMDALNIFIRIAIILAGD------QKRKN 365
                                                                                                                                  Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George K., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Submitter S.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY072204, AAL68072.1; --
SEQUENCE 365 AA, 39108 MW, 676C61176F923745 CRC64;
                                                                                                               198 EIIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILIIMLKNASEKEEKKKKRRN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%; Score 192; DB 5; Length 365; 25.7%; Pred. No. 5.6e-09; Live 49; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative TEGT family carrier/transport protein.
                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                       01-010N-2002 (TrEMBLrel. 21,
01-010N-2002 (TrEMBLrel. 21,
01-010N-2002 (TrEMBLrel. 21,
4714090p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
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NCBI_TaxID=602
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Best Local S
Matches 61
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Q8ZQ61;
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RESULT 10 Q8ZQ61

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STRAIN-BERKELEY;

XX MEDINE=21946066; PubMed=10731132;

Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Accorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

April J.F., Agbayani A., An H.-J., Andrawe-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Barnelle J., Bayraktaroglu L., Beaaley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Beeson K.Y., Benos P.V., Berman B.P., Brotter P.,

Beeson K.Y., Busam D.A., Buller H., Gadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Acherry J.M., Cawley S., Dahlke C., Davenport S., Dunkov B.C., Dunn P.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleitschmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M. Sanderson K. B., Spicth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C.; Scott K., Holmes A., Grewal N., Mulvaney E., Ryan F., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Perygota, Neoptera, Endopteryota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 -TYKTANKPVGILSAFAFTGFLGYILGPILNAYLSAGMGDVJGLALGGTALVFFCCS-AY 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 RQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLLTTWACMGSMVWLLSA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 MLARREYLYLGGLLSSGVSLLF------WLHFASSIFGGSMAVFKFELYFGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 RDRSSLLSTHKVLRNTYFLLSLTLALSAITATASTVLMLPSPGLILTLVGMYGLMFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 174.5; DB 16; Length
29.6%; Pred. No. 1.1e-07;
tive 42; Mismatches 76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein, Complete proteome.
SEQUENCE 219 AA; 23313 MW; 9FA28BACE70B8497 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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SEQUENCE FROM N.A.
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Q8Z7R5
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez Jr., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J. Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
Reinert K., Remington K.S., Pan S., Pollard J., Purl V., Reese M.G.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleon M., Strong R., Sun E.,
Nang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.),
We J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Morse E.W., Rubin G.M., Venter J.C.;
Ciben R.A., Myers E.W., Rubin G.M., Venter J.C.;
Riybase, PBGN030263, CG2076.
Riybase, PBGN030263, CG2076.
RinterPro, IDPR00127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 IGLGVVFASSLASMWLPPTTALGAG---LASMSLYGGLVLFSGFLLYDTQRWVRRAEVYP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MN-2002 (TrEMBLrel. 21, Last annotation update)
Growth hormone-inducible membrane protein (Similar to PTD010 protein)
(Hypothetical 37.3 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 MAAALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li Y., Kelder B., Kopchick J.J.;
"Identification, isolation, and cloning of growth hormone (GH)-inducible interscapular brown adipose complementary deoxyribonucleic acid from GH antagonist mice.";
Endocrinology 142:2937-2945(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 CVLTAAAAAATFRSHRLLELASRGGILATIASLALVIGSGAVARSIEYQPGLGAKHLAWA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 CALVASAAGAYL--HILWNI---GGLLTTWACM-----GSMVWLLSAPPYQEQKRVALL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 172; DB 5; Length 341; llarity 26.5%; Pred. No. 3e-07; Conservative 46; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prem; PF01027; UPF0005; I.
SEOUENCE 341 AA; 35817 MW; 7A2AB68A8C6A5525 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 QYSYTPYDPINASMSIYMDVLNIFIRIVTIL 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
MEDLINE=21308975; PubMed=11416014;
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es 56; Conserv
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamiln M., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterior servor Typhic (T18.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 VSLLFWLHFASSIFGGSM-----AVFKFELYFGLLVFVGYIVFDTQEIIEKAHLG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AALFEGASIGPLIELGINFDPSIVFGAFVGCAVVFGCFSAAAMLARREYLYLGGLLSSG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
13.4%; Score 171; DB 11; Length 346;
Best Local Similarity 25.9%; Pred. No. 3.7e-07;
Matches 57; Conservative 47; Mismatches 84; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 170.5; DB 16; Length 219;
                                                                                                                 Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF412297, AALO7803.1; -.
EMBL; BC008622; AAH08622.1; -.
EMBL; BC010224; AAH10224.1; -.
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:848-852(2001).
EMBL, AL627269, CAD08212.1;
Pfan, PF01027; UPF0005; L.
PROSTITS, PS01243; BII, UNKNOWN I.
PROSTITS, PS01243; BII, UNKNOWN I.
HYPOTHELICAL DYCLEIN; COMPLETE DYCHEOME,
SEQUENCE 219 AA; 23347 MW; 914661A809EF6E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       l protein.
346 AA; 37275 MW; 1CFB22B2612BB70D CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 DM-----DYVKHALILFIDFGAVFVRILLIMLKNASEKE 240
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                                                                                                                                                                                                                                                                       MGD; MGI:1913342; Ghitm.
InterPro; IPR002199; Bax inhbtrl.
Pfam; PF01027; UPF0005; Ī.
Hypothetical protein.
SEQUENCE 346 AA; 37275 MW; IC
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Query Match
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              11;
                                                                                 83 PPYQ-EQKRVALLMAAAL--FEGASIGPLIELGINFDPSIVFG-AFVGCAVVFGCFSAAA 138
                                                                                                19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHILMNI--GGLLTTMACMGSM 76
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                                                     9 RDRSSLLSTHKVLRNTYFLLSLTLAFSAITATASTVLMLFSFGLLTLVGMYGLMFL-- 65
              Gaps
                                   ROISPLVOTH--LKQVY--LTLCCALVASAAGAYLHILWNIGGLLTTMACMGSMVWLLSA 82
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
Winteroe A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine CDNA
                                                                                                                                                Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                 139 MLARRREYLYLGGLLSSGVSLLF------WLHFASSIFGGSMAVFKFELYFGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 164; DB 6; Length 99; 36.3%; Pred. No. 4e-07; ive 19; Mismatches 35; Indels
              77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81159; CAB03546.1; -
InterPro; IPR002199; Bax_inhbtr1.
Pfam; PF01027; UPF0005; I.
NON_TER
                                                                                                                                                                                187 VFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
                                                                                                                                                                                                99 AA; 10846 MW; EA009C94B5EE6211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative carrie/transport protein.
YCCA OR Z1222 OR ECS1054.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
 ; Pred. No. 2.5e-07; 42; Mismatches 77
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   29.2%;
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Best Local Similarity 36.33
Matches 33; Conservative
               66; Conservative
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Best Local Similarity
Matches 66; Conserv
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NCBI_TaxID=83334;
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01-JUN-2002
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Q95309
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SECURIOR SECURIOR NO. 1 RIND 0509952;

STRAIN=0157:H7 RIND 0509952;

MEDLINE=1115631; PubMed=11258796;

MEDLINE=1116231; PubMed=11258796;

MEDLINE=1116231; PubMed=11258796;

MID HAN C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T.,

MA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.; Shinagawa H.;

Complete genome sequence of enterchemorrhagic Escherichia coli

T. Complete genome comparison with a laboratory strain K-12.";

MA Res. 1811-22001)

EMBL; AR05254; BAB34477.1;

DR EMBL; AR052554; BAB34477.1;

TINCEPPO; IPRO0199; Bax inhbr1.

PRESTIE: PS01243; BII; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VGCAVVFGCFSAAAMLARRREYLYLGGLLSSGVSLLF------WLHFASSIFGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 SMAVEKFELYFGLLVFVGYIVFDTQEIIEKAHLGDMDYVKHALTLFTDFGAVFVRILIIM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TIMACMGSMVWLLSAPPYQEQKRVALLMAAAL--FEGASIGPLIELGINFD-PSIVFGAF 124
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074335; PubMed=11206551;
MEDLINE=21074335; PubMed=11206551;
Rose D.J., Plunkett G. III. Burland V., Mau B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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12.4%; Score 157.5; DB 16; Length
Local Similarity 26.7%; Pred. No. 3.5e-06;
hes 64; Conservative 45; Mismatches 80; Indels
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Job time : 61 secs
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SEQUENCE 219 AA;
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